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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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OM protein - protein search, using sw model

November 21, 2002, 13:40:47; Search time 11 Seconds (without alignments) 203.611 Million cell updates/sec Run on:

US-09-776-724A-142

1 MRRCVRHVLGIGLIVLKNLY......FQEAFLFFFLILKNPLTLCS Perfect score: Sednence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Potal number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	pti	P53245 saccharomyc		_	P42391 buchnera ap	P47774 mus musculu		escherichi	P53379 saccharomyc		P16757 human cytom		schiz			vaccinia			014164 homo sapien	schiz						O66932 aquifex aeo		_		Q09291 caenorhabdi		_	P40144 oryctolagus	P21783 xenopus lae
SUMMARIES	ID	YG2C_YEAST	O2A4_HUMAN	YG64_YEAST	TRPB_BUCAP	CKR7_MOUSE	YRU5_CAEEL	MDOC_ECOLI	MKC7_YEAST	YIJ2_YEAST	UL16_HCMVA	AQP5_HUMAN	CGM2_SCHPO	ADT1_GOSHI	VP4B_VACCV	VP4B_VACCC	OSTG_YEAST	TR11_FUSSP	IKKE_HUMAN	YAQ5_SCHPO	PAHX_BOVIN	CKR7_HUMAN	C135_DROME	VP4B_VARV	NCPR_CAVPO	PHSG_AQUAE	MUTT_BUCAI	ADT2_YEAST	YNN2_YEAST	YQL2_CAEEL	PHYA_ARATH	CYA5_RAT	CYA5_RABIT	NOTC_XENLA
	DB																										-	Н						_
	Length	111	310	153	399	378	363	385	296	633	230	265	322	386	643	644	350	492	716	2670	337	378	487	644	677	692	124	318	1056	367	1122	1262	1264	2524
ф	Query Match	21.2								19.1		18.7	18.7	18.7	18.7	18.7	18.6	18.6	18.6	18.6	18.4	18.4	18.4	18.4	18.4	18.4	18.2	18.2	8	8	œ	8	18.0	20
	Score	09		56.5	•		ഗ	55.5	~	54	53	53	53	53	23	53	52.5	52.5	52.5	52.5	52	52	52	52	52	52	51.5	51.5	51.5	51	51	51	51	ΣŢ
	Result No.	-	7	m ·	4	ഗ	9	7	30 (ο,	OT.	II	12	13	14	15	16	17	18	19	20	$\frac{21}{21}$	22	23	24	25	52	27	28	67	30	31	32	33

											homo sapien
P53561	P49382	068428	051653	P40453	014832	P51477	P49185	P45983	P39373	P48921	P16435
YTCP BACSU	ADT_KLULA	TRPB_BUCDN	PRIM_BORBU	UBP7_YEAST	PAHX_HUMAN	ARRS XENLA	MK08_RAT	MK08_HUMAN	GNTP_ECOLI	NU5M_FELCA	NCPR_HUMAN
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286	305	397	523	1071	338	396	411	427	447	909	9/9
17.8	17.8	17.8	17.8	17.8	17.7	17.7	17.7	17.7	17.7	17.7	17.7
		50.5 17.8			•	•		` '		, ,	

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 6
                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 13.6 kDa protein in VHTI-ROM1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.2%; Score 60; DB 1; Length 111; 34.0%; Pred. No. 0.63; Live 5; Mismatches 20; Indels
                                                                                                                                                                                                                                     Wedler H., Scharfe M., Wedler E., Wambutt R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-PHE.
161DE34E1D75AAEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
                 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SGD; S0003301; YGR069W.
Hypothetical protein; Transmembrane.
TRANSMEM 27 47 POTENTIAL.
                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AA; 13603 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z72853; CAA97071.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Conservative
                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olfactory receptor 2A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=4932;
               YG2C_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O2A4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
O2A4_HUMAN
YG2C_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Keast 13:251-259(1997).
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                                   Watson M.D.;
                                                                                                                                                                                                                                                                                                                                                  52 LCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                  TRPB_BUCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        graminum)
                                                                                                                                                                                                                                 SEQUENCE
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                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Volckaert G., Voet M., Robben J.;
"Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the right arm of chromosome VII from Saccharomyces cerevisiae carrying the MAL1 locus reveals 15 complete open reading frames, including 2001, BGL2 and BIO2 genes and an ABC transporter gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
            Hou S., Wohldmann P., Le T.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: PUTATIVE ODORANT RECEPTOR.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Very hypothetical 17.3 kDa protein in MALIS-COS6 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 RICESHLCVIGLVYGTAIIMYVGPRYGNPK---EQKKYLLLFHSLFNPMLNPLICS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL). 8C4F26BBB55C8D7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.8%; Score 59; DB 1; Length 310; 30.4%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Indels
                                                                                                                                                                                                                               PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                           1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                     5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                          3 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
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                                                                                                                                                                                               InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288c / FY1679;
MEDLINE=97245295; PubMed=9090054;
                                                                                                                                                                            EMBL; AC005587; AAD05193.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34802 MW;
                                                                                                                                                                                                                                                                     Multigene family; Olfaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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78
99
1119
1138
1157
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                                                                                                                                                                                       HGNC:14729;
   SEQUENCE FROM N.A.
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49
57
79
100
120
139
158
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P53342;
                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                             FRANSMEM
                                                                                                                                                                                                                                                                                                                   TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-! FUNCTION: THE BETA SUBUATI IS RESPONSIBLE FOR THE SYNTHESIS

-! FUNCTION: THE BETA SUBUATI IS RESPONSIBLE FOR THE SYNTHESIS

-! CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate + H(2)0.

-! COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

-! PATHWAY: TIYPTOPAN biosynthesis; fifth (last) step.

-! SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY SIMILARITY).

-! SIMILARITY: BELONGS TO THE TRPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RCVRHV---LGIGLIVLKNLYFHKNSM-----YPSPKLSSFQEAFLFFFLILKNPLF 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-94012512; PubMed-8407819;
Munson M.A., Baumann P.;
"Molecular cloning and nucleotide sequence of a putative trpDC(F)BA operon in Buchnera aphidicola (endosymbiont of the aphid Schizaphis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 153;
                                                                        Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBL_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.; 75652655DBCC01E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophan synthase beta chain (EC 4.2.1.20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.0%; Score 56.5; DN Best Local Similarity 27.0%; Pred. No. 2.5; Matches 17; Conservative 11; Mismatches
                                                                                                                 -!- SIMILARITY: STRONG, TO YEAST YBR300C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 AA; 17314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z73078; CAA97326.1; -. SGD; S0003525; YGR293C.
SEQUENCE OF 1-13 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 7 precursor (C-C CKR-7) (CC-CKR-7) (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6 X CBA; TISSUE-Thymus; MEDLINE=95154835; PubMed=7851893; Schwelckart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr., Sthows T.B., Gray P.W.; "Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor encoded on human chromosome 17q12-q21.2."; Genomics 23:643-650(1994).
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                             TIGRFAMS; TIGRO0263; LTPB; 1.

PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.

Tryptophan biosynthesis; Pyridoxal phosphate; Lyase.

BINDING 86 86

SRQUENCE 399 AA: 44247 MW; DEBFD45D2C859C30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000276; GPCR_Rhodpsn.
Pram; PF00001; 7tm_l; 1.
PRNWTS: PR00037; GPCRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL
FOTENTIAL.
FOTENTIAL.
                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                     Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-C CHEMOKINE RECEPTOR TYPE 7. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                                                                                                                                                             14 IVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKN-----PLTLCS 54
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                        20.0%; Score 56.5; DF 36.2%; Pred. No. 6.4; tive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 AA
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                                         InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000993; Trp_synth_beta.
Pfam; PF00291; PALP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR CMKBR7 OR EBIL OR EBILH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
EMBL; Z19055; CAA79500.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L31580; AAA74232.1; -.
                                                                                                                                                                                                                                                                                 Local Similarity 36.2 nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:103011; Cmkbr7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                          HSSP; P00933; 2WSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKR7_MOUSE
P47774:
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRANSMEM
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  DR RW KW KW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 VRHVLGIGLIVLK---NLYFHKNSMYPSPK------LSSFQEAFLFF-FLILK 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 VEMILAVGCLIMNTNITVICHKASPMPHPQRRLLASISINFAILSGFQLARNFFLFLVMQ 84
                                                                                                                    7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.6%; Score 55.5; DB 1; Length 363; 29.0%; Pred. No. 7.9; Live 10; Mismatches 17; Indels 17
                                                                                                                                                                                                                               19.8%; Score 56; DB 1; Length 378;
                                                                                                                                                                                                                                                                22; Indels
                  EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                               ACB1A422CF54AA54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
7389680068BAFCB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0707-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 40.9 kba protein T09B9.5 in chromosome X.
 CYTOPLASMIC (POTENTIAL).
                                                   5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                   69 CFVGLEGNGLVILTYIYFKRLKTMTDTYLLNLAVADILFLLIL 111
                                                                                                                                                                                                                                                                                                 4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                               Pred. No. 7; 7; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             363 AA
                                                                                                                                                                             BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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Hypothetical protein; Transmembrane
                                                                                                                                                                                          42941 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40964 MW;
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                                                                                                                                                                                                                                               32.6%;
                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
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206
247
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332
36
129
378 AA;
                                                                                                                                                                                                                                             Similarity
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186
227
268
363 AA;
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153
171
192
220
248
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Best Local Simi
Matches 18;
                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                      YRUS_CAEEL
ID YRUS_CAEEL
AC Q09351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kershaw J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 NP 49
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DOMAIN
TRANSMEM
                                   DOMAIN
TRANSMEM
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Best Local
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SEQUENCE
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                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The mdoc gene of Escherichia coli encodes a membrane protein that is required for succinylation of osmoregulated periplasmic glucans.";
J. Bacteriol. 181:3624-3631(1999).
-!- FUNCTION: NECESSARY FOR THE SUCCINYL SUBSTITUTION OF PERIPLASMIC GLUCANS. COULD CATALYZE THE TRANSFER OF SUCCINYL RESIDUES FROM THE CYTOPLASMIC SIDE OF THE MEMBRANE TO THE NASCENT GLUCAN BACKBONES ON THE PERIPLASMIC SIDE OF THE MEMBRANE.
-!- PATHWAY: OPG (OSMOREGILATED PERIPLASMIC GLUCANS) BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Santo N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                         STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99296569; PubMed-10368134;
Lacroix J.-M., Lanfroy E., Cogez V., Lequette Y., Bohin A.,
Bohin J.-P.;
                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                              15-UUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                               385 AA
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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                               PRT;
                                                                                                            Glucans biosynthesis protein mdoC. MDOC OR B1047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000206; AAC74131.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D90741; BAA35837.1; -. D90742; BAA35845.1; -.
                               STANDARD;
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80
111
157
157
233
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D90742;
                                                                                                                                                                                         Escherichia
              MDOC_ECOLI
ID MDOC_ECOLI
AC P75920;
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TRANSMEM
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=96068694; PubMed=7479877; Komano H., Fuller R.S.; "Shared functions in vivo of a glycosyl-phosphatidylinositol-linked aspartyl protease, MkC7, and the proprotein processing protease Kex2 in yeast.";
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S288c / AB972;
Murphy L., Richards C., Harris D., Barrell B.G., Rajandream M.A.,
                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aspartic proteinase MKC7 precursor (EC 3.4.23.41) (Yapsin 2).
MKC7 OR YDR144C OR YDB358.01C OR YD2943.03C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycetes;
                                                                                                         1;
                                                                           Query Match
Best Local Similarity 31.1%; Pred. No. 8.3;
Matches 14; Conservative 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                    24B869CE8E0224DF CRC64;
                                                                                                                                                  281 VLGLWMVNVVFSFGHRLLNFQSARVTYFVNASLFIYLV-HHPLTL 324
                                                                                                                                 8 VLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                                                                     Sacchāromycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 92:10752-10756(1995).
            POTENTIAL. POTENTIAL.
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MENUCY.
InterPro; IPR001461; AspproteaseAl.
InterPro; IPR001969; Aspprotease_site.
                                       POTENTIAL
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EMBL; Z50046; CAA90357.1; -.
EMBL; Z54139; CAA90813.1; -.
HSSP; P32329; IXPS.
MEROPS; A01.031; -.
                                                      44690 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 188-596 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-196 FROM N.A.
                                                                                                                                                                                                                                  STANDARD;
 259
294
331
358
239
274
211
311
338
385 AA;
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P53379:
  TRANSMEM
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Pfam; PF00026; asp; 1.

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                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parall B.G. Badcock K., Bankier A.T., Bowman S., Brown D., Barrell B.G., Badcock K., Dankier A.T., Dear S., Devlin K., Fraser A., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A., Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                  ASPARTIC PROTEINASE MKC7.
REMOVED IN MATURE FORM (POTENTIAL).
                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                   (POTENTIAL)
                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                      (POTENTIAL)
                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                        6
           PROSITE; PS00141; ASP_PROTEASE; 2.
Hydrolase; Aspartyl protease; Glycoprotein; Signal; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 71.0 kDa protein in SGA1-KTR7 intergenic region.
                                                                                                                                                                                                                                                                                                 DB 1; Length 596;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                          A3C7CF5770A922BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
7B9279E345D4F656 CRC64;
                                                                                       BY SIMILARITY.

N-LINKED (GLCNAC...)

POLY-SER.
                                                                                                                                                                                                                                                                                                                                                        237 VLGIGLPGLE-----STYSGVSLSSVQKSYTYNNFPMVLKN 272
                                                                                                                                                                                                                                                                                                                                           8 VLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLF--FFLILKN 48
                                                                                                                                                                                              (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                           Pred. No. 17;
7; Mismatches 10;
                                                                                                                                                                                                                                                    A -> T (IN REF. 3).
P -> T (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                         633 AA
                                                                                                                                                                                                                                                                                                Score 54.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGD; S0001354; YIL092W.
Hypothetical protein; Transmembrane.
FRANSMEM 99 118 POTENTIAL.
                                                         POTENTIAL.
                                                                                                                                                                                                                                                                          64235 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71006 MW;
                                                                                                                                                                                                                                                                                                19.3%;
39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z46728; CAA86702.1; -.
                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
PRINTS; PR00792; PEPSIN
                                            22
65
65
575
596
360
1180
129
223
232
232
286
                                   GPI-anchor; Zymogen.
                                                                                                                                                                                                                                                                          596 AA;
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           633 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                       23
66
576
99
360
1180
219
229
232
286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                         YIJ2_YEAST
                                                                            PROPEP
ACT_SITE
                                                                                                   ACT_SITE
CARBOHYD
                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                          CARBOHYD
                                                                                                                          CARBOHYD
                                                                                                                                    CARBOHYD
                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                            SIGNAL
                                                       PROPEP
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                P40497
                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                             YIJ2_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
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A MEDLINE-90269039; PubMed=2161319;
A MEDLINE-90269039; PubMed=2161319;
A Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
A Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
A horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
A horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
A horsnell T., Hutchison C.A. Tomlinson P., Weston K.M., Barrell B.G.;
A horsnell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
A preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
A horsnell State ADLE C., Tomlinson P., Weston K.M., Barrell B.G.;
Curr. Top. Microbiol. Immunol. 154:125-169(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches 16; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 VLKNLYFHKNSMYP-----SPKLSSFQE------AFLFFFLILKNPL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                             4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
            DB 1; Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26147 MW; B72F2C241C569967 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                       15;
                                                                                                                                                                                           286 KKNYFDKNSQHIPDPKRRKQNEPGMRLFLVMDEEKNILT 324
                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                 17 KNLYFHKNSMY-PSPKLSSFQEAFLFFFLIL---KNPLT
                                                                                                                                                                                                                                                                                                                                                       230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 AA.
                                      Pred. No. 21;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 34, Created)
(Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
            Score 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X17403; CAA35448.1; -. PIR; S09778; S09778.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.7%;
23.8%;
                                          41.0%;
Query Match
Best Local Similarity 41.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein UL16
                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
95
101
132
145
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P55064;
01-OCT-1996 (
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                                                                                                                                                                                                                                                                                                                                                UL16_HCMVA
P16757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
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AQP5_HUMAN
ID AQP5_HU
AC P55064;
DT 01-OCT-
DT 01-OCT-
                                                                                                                                                                                                                                                                                                                      UL16_HCMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 LSIGLSVTLGHLVGIYFTGCSMNPARSFGPAVVMNRFSPAHWVFWVGPIVGAVLAAILYF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 12;
8; Mismatches 17; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=96224064; PubMed=8621489;
Lee M.D., Bhakta K.Y., Raina S., Yonescu R., Griffin C.A.,
Copeland N.G., Gilbert D.J., Jenkins N.A., Preston G.M., Agre P.;
"The human Aquaporin-5 gene. Molecular characterization and chromosomal localization.";
                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 271:8599-8604 (1996).
-!- FUNCTION: FORMS A WATER-SPECIFIC CHANNEL. IMPLICATED IN THE GENERATION OF SALIVA, TEARS, AND PULMONARY SECRETIONS.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.7%; Score 53; DB 1; Length 265; 27.1%; Pred. No. 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U46569; AAC50474.1; -.
EMBL; U46566; AAC50474.1; JOINED.
EMBL; U46567; AAC50474.1; JOINED.
EMBL; U46568; AAC50474.1; JOINED.
HSSP; P29972; 1H61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00783; MINTRINSICP.
ProDom; PD000295; MIP_family; 1.
TIGREAMS; TIGRO0861; MIP; 1.
PROSITE; PS00221; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000425; MIP_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28292 MW;
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Watches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:638; AQP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00230; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
162
183
206
227
124
125
265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|: | 1:|
223 YLLFPNSLSL 232
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                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 600442;
                          Aquaporin 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43
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DDA BERTHER FEETE FEETE
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RESULT 12

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WEDELINE-21848401; PubbMed=11859360;

WEDELINE-21848401; PubbMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Bodouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gollins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgeon G.,

RA Gollins M., Dones L., Jones M., Leather S., McDonald S., McLean J.,

RA Holroyd S., Honnels M., Leather S., McDonald S., McLean J.,

RA Holroyd S., Woule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Diver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,

RA Cliver K., O'Neil S., Rounders D., Seeger K., Stevens K.,

RA Relton J., Simmond M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whithehead S.,

RA Taylor K., Taylor R.G., Aert R., Robben J., Grymonprez B.,

RA Taylor K., Taylor R., Fitzc C., Helzer E., Moestl D., Hilbert H.,

RA Gabel C., Fuchs M., Fitzc C., Helzer E., Moestl D., Hilbert H.,

Borzym K., Langer I., Beck A., Iehrach H., Reinhardt R., Pohl T.M.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

A Lucas M., Rochet M., Gaillardin C., Moore K., Hurst S.M.,

Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

Rybonniquez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.,

Rybonniquez A., Beyden P., Barrell B.G., Nurse P.;

Rybonniquez A., Beyden PROGRESSION THROUGH THE CELL CYCLE.

PROBABLY INTERPACTS WITH A PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           MEDINE-93223713; PubMed-8467814; Molz L., Beach D.; "Characterization of the fission yeast mcs2 cyclin and its associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                Cyclin mcs2 (Mitotic catastrophe suppressor 2)
                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
322 AA
                                                                                                                                                          pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00134; cyclin; 1.
SMARY; SM00385; CYCLIN; 1.
TGRPAMS; TIGRO0569; ccll; 1.
PROSITE; PS00292; CYCLINS; FALSE_NEG.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL441603; CAC08541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S59895; AAB26193.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P51946; 1KXU.
InterPro; IPR005258; Ccll.
InterPro; IPR004366; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                              protein kinase activity.";
EMBO J. 12:1723-1732(1993).
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S35380; S35380.
                                                                                                                                     MCS2 OR SPBP16F5.02.
                                                                                                                                                                                                                             Schizosaccharomyces.
                                                                                                                                                            Schizosaccharomyces
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                NCBI_TaxID=4896;
  CGM2_SCHPO
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                         P36613;
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PROPEP
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          VP4B_VACCV
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                                                            ö
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. Texas Marker 1; TISSUE=Fiber;
Shin H., Brown R.M. Jr.;
"Two CDNA sequences for the adenine nucleotide translocator, CANT1 and CANT2, from cotton fibers (Gossypium hirsutum).";
(In) Plant Gene Register POR97-130.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                           Gossypium hirsutum (Upland cotton).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00215; MITOCH_CARRIER; 2.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
Transit peptide; Multigene family:
TRANSIT 1
MITOCHONDRION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 VGIIVYRGLYF---GMYDSLKPVLLTGSMQDSFFASFVLGWLITNGAALAS 309
                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP.ATP carrier protein 1, mitochondrial precursor (ADP/ATP
translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                           inner membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOCHONDRION (BY SIMILARITY). ADP, ATP CARRIER PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 386;
18;
                                    18.7%; Score 53; DB 1; Length 322,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 IGLIVLKNLYFHKNSMYPSPK----LSSFQEAFLFFFL---ILKNPLTLCS
                                                             18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A05F76C73FECDEE6 CRC64;
Cyclin; Cell cycle; Cell division; Nuclear protein. SEQUENCE 322 AA; 37673 MW; 09B8DDB46563727C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                     8; Mismatches
                                                32.4%; Pred. No. 15; ive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                     7 HVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.7%; Score 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42093 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF006489; AAB72047.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%;
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                                                             11; Conservative
                                                                                                                                                                            STANDARD;
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386
107
170
212
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hes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 AA;
                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3635;
                                                                                                                                                                            ADT1_GOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                      Query Match
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                                                               Matches
                                                                                                                                                   RESULT 13
ADT1_GOSHI
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                                                                                                                                                                                                                                                                                                                                                                                    and nucleotide sequence
the precursor of the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        van Slyke J.K., Franke C.A., Hruby D.E.;
"Proteolytic maturation of vaccinia virus core proteins:
identification of a conserved motif at the N termini of the 4b and
25K virion proteins.";
J. Gen. Virol. 72:411-416(1991).
-!- FUNCTION: PRECURSOR FOR ONE OF THE TWO MOST ABUNDANT STRUCTURAL
COMPONENT OF THE VIRION (MAJOR CORE PROTEINS 4A AND 4B).
                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Major core protein P4b precursor (Virion core protein P4b).
                                              01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Major core protein P4b precursor (Virion core protein P4b).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.7%; Score 53; DB 1; Length 643; 29.5%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1989) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q -> N (IN REF. 2).
6F073332BAFD0E59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAJOR CORE PROTEIN P4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 VLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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                                                                                                                                                                                                                                                                                                                                                                                 "Transcriptional and translational mapping analysis of a vaccinia virus gene encoding core polypeptide 4b.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 62-70.
MEDLINE=91132139; Pubmed=1993877;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=86062913; PubMed=2999438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           643 AA; 72498 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A03871; FOVZZW.
InterPro; IPR004972; Pox_P4B.
Pfam; PF03292; Pox_P4B; 1.
Core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M11079; AAA48298.1; -. EMBL; M27914; AAA48303.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virol. 56:830-838(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 1-201 FROM N.A.
                                                                                                                                                                                 Vaccinia virus (strain WR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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STANDARD;
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                   Rosel J., Moss B.;
                                                                                                                                                                                                                                                           NCBI_TaxID=10254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
62
122
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VP4B_VACCV
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CONFLICT
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                                                                                                                                                                                                                                                                                   "Appendix to 'The complete DNA sequence of vaccinia virus'.";
Virology 179:517-563(1990).
-!- FUNCTION: PRECURSOR FOR ONE OF THE TWO MOST ABUNDANT STRUCTURAL
COMPONENT OF THE VIRION (MAJOR CORE PROTEINS 4A AND 4B).
Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                           SEQUENCE FROM N.A.
MEDLINE-91021027; PubMed=2219722;
Goebbel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
                                                                                                                                                                                                                                                   Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P., Paoletti E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.7%; Score 53; DB 1; Length 644; Best Local Similarity 29.5%; Pred. No. 29; Matches 13; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
MAJOR CORE PROTEIN P4B.
76CC2ED6781F88A2 CRC64;
                                                                                                                                                                        "The complete DNA sequence of vaccinia virus."; Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROPEP 1 61 B
CHAIN 62 644 M.
SEQUENCE 644 AA; 72624 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M35027; AAA48118.1; -.
PIR; E42517, FOVZE,
Interpro; IPR004972; POX_P4B.
Pfam; PF03292; POX_P4B; I.
                                                        NCBI_TaxID=10249;
                                                                                                                                                                                                                                 COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Core protein.
PROPEP
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ö

Gaps

0;

8 VLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLT 51

ò g Search completed: November 21, 2002, 13:41:50

Job time : 13 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein . protein search, using sw model

November 21, 2002, 13:40:47; Search time 29 Seconds Run on:

(without alignments) 383.674 Million cell updates/sec

US-09-776-724A-142 Perfect score:

I MRRCVRHVLGIGLIVLKNLY......FQEAFLFFFLILKNPLTLCS 54 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:* Database :

_unclassified:* sp_human:*
sp_invertebrate:*
sp_mammal:* sp_vertebrate:* sp_bacteriap:* sp_archea:*
sp_bacteria:*
sp_fungi:* sp_organelle:* rodent: * sp_rvirus:* sp_plant:* sp_virus:* sp_phage: sb_mhc:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

026431 methanobact 09ngn0 homo sapien 0918c2 xenopus lae 024437 oryza longi Q9bb33 chondrorhyn Q9bb38 dichaea neg Q24788 echinococcu Q8ss65 encephalito Q9stw2 arabidopsis 082159 populus nig 09bb39 dichaea mur Q8zhg6 yersinia pe Q9bb34 cryptarrhen Q9c4y2 sulfolobus 095bp4 pescatorea 09bb32 pescatorea Description SUMMARIES Q9NQN0 Q9I8C2 024437 082159 Q9STW2 98ZHG6 Q9BB39 Q9BB32 Q9BB33 Q95BP4 Q9BB38 186 Query Score Match Length DB 20.7 20.5 20.5 20.5 20.5 20.5 20.5 20.5 20.3 20.3 58.5 58.5 58 58 58 58 58 58 57 57 No. 5 6 7 10 11 11 11 11 11 11 11 11 11

Q9C4Y2

094736 stomoxys ca 093552 carassius a 08wf21 bhutanitis 09yv20 melanoplus 08tht5 methanosarc	Q9bb37 warrea warr Q9lp15 arabidopsis Q9zt57 arabidopsis	Q8y814 listeria mo Q92dd2 listeria in		O9xyr3 caenorhabdi	Ogémes homo sapien			Q91cpi tupaia nerp Q9baz7 soterosanth	× ×	25	ຜວ	O/O481 mus musculu
Q94736 3 Q93552 Q8WF21 2 Q9YVZ0 7 Q8THT5	8 Q9BB3/ 10 Q9LPL5 10 Q9ZT57	6 Q878L4 6 Q92DD2 09RMC9	7 Q9YAG6 09B601	Q9XWR3	096MA5 08x916		2 Q8UZ09	90		C	_	
678 5 844 1 119 8 177 1 225 1						458 13 1146 12					675 5	
20.0 20.0 19.8 19.8	110.00	19.8	19.8 19.6	19.6 19.6	19.6 19.6	19.6 19.6	19.6 19.6	19.4 19.4	19.4	19.3 19.3	19.3	
56.5 56.5 555 556 566	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	56 56	5.	. n	55.5	м. М	. i.	5 5 5 5	55 55	44	54.5 54.5	
118 118 220 221	222 243 243	26	5 8 7 8	30 31	35 33	34 35	36 37	8 6 3 6	40 41	42	44 45	

ALIGNMENTS

01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
101-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 45.7 kDa protein.
172A6.150 OR A44GA4320
Arabidopsis thaliana (Mouse-ear cress).
Eukaryotta, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II: Brassicales; Brassicaceae; Arabidopsis. Limmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P., Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. [1]
SEQUENCE FROM N.A.
BEVARD M., ZIMMETMARD W., Grueneisen A., Wambutt R., Bancroft I.,
Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EU Arabidopsis sequencing project; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. Ed Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO79637; CAB45067.1;
EMBL; ALO71651; CAB75942.1;
InterPro: IPR002203; Intein.
PROSITE: PS00881; PROTEIN_SPLICING; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 395 AA; 45690 MW; EA8CE0F16E1E806D CRC64; 395 AA. PRT; PRELIMINARY; SEQUENCE FROM N.A. SEQUENCE FROM N.A. Q9STW2 RESULT 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RRCVRHVLGIGL------39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-UNN-2000 (TrEMBLrel. 17, Last annotation update)
011005411.1 (7 transmembrane receptor (Rhodopsin family) (Olfactory receptor like) (Fragment).
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                     4;
                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.2%; Score 60; DB 17; Length 221; 30.9%; Pred. No. 5.6;
                                                                                       4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSS----FQEAFLFFFLILKNPL 50
Score 63; DB 10; Length 395;
Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                     8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 179:7135-7155(1997).

EMBL, AE000818; AAB8487.1; -.

Interpro; IPR001173; Glycos_transf_2.

Pfam, PF00535; Glycos_transf_2? 1.

Transferase; Glycosyltransferase; Complete proteome.

SEQUENCE 221 AA; 24710 NW; 96B0E95F98081A09 CRC64;
                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MANNOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 5.6;
8; Mismatches
                                                                                                                                                                                          221 AA
                                                                                                                                                                                                                                                                                                             Methanobacterium thermoautotrophicum.
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                                                                                                                                                                                            PRT;
        22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                            Best Local Similarity 33.39
Matches 17; Conservative
                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 IFRTLVLE 218
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 LFFFLILK 47
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-DELTA H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DJ1005H11.1
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               Query Match
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01-JAN-1998 (TIEMBLrel. 05, Last sequence update)
01-JAN-1998 (TIEMBLrel. 05, Last annotation update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
Receptor kinase-like protein.
0ryza longistaminata (Long-staminate rice).
0ryza longistaminata (Long-staminate rice).
Spermatophyta; Virialplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae: Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Kanopus Ametazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                   200 RTCFSHLCVIGLVYGTAIIMYVGPRYGNPK---EOKKYLLLFHSLFNPMLNPLICS 252
                                                                                                                                                                                    2 RRCVRHULGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.7%; Score 58.5; DB 13; Length 325; 28.3%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 CVRHVLGIGLIVLKNLYFHKNSMYP---SPKLSSFQEAFLFFFLILKNPLTLC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Two classes of olfactory receptors: molecular and functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28; Indels
                                                                                                                         20.8%; Score 59; DB 4; Length 272; 30.4%; Pred. No. 9.2;
                                                                                                                                                           24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 AA; 37075 MW; 94CDE3DC322C97A4 CRC64;
                                                                                       NON_TER 1 1 1
SEQUENCE 272 AA; 30452 MW; 4FF5CF18077574CD CRC64;
                                                                                                                                                                                                                                                                                                                                  01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0UN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               612 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                                                                             9; Mismatches
EMBL; AL135904; CAB99212.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PR0001; Tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AJ250752; CAC00723.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=IRBB21;
MEDLINE=96106403; PubMed=8525370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-OLFACTORY EPITHELIUM; Mezler M., Breer H.;
                                                                                                                                                 30.4%;
                                                                                                                                                                                                                                                                                                                                                                                       Olfactory receptor class I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                             Best Local Similarity 30.49
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM. N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
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1;
Song W.Y., Wang G.L., Chen L.L., Kim H.S., Pi L.Y., Holsten T., Gardner J., Wang B., Zhai W.X., Zhu L.H., Fauquet C., Ronald P.; "A receptor kinase-like protein encoded by the rice disease resistance qene, Xa21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Populus nigra (Lombardy poplar).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                    Song W.Y., Pi L.Y., Wang G.L., Gardner J., Holsten T., Ronald P.C.;
"Evolution of the rice Xa21 disease resistance gene family.";
Plant Cell 9:1279-1287(1997).
EMBL: 072726; AABB2753.1;
InterPro: IPR001511; LR.
InterPro: IPR001502; LRR. out.
Pfam; PF00560; LRR: 21.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00370; LRR: 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishiguchi M.;
"A cDNA clone encoding cytosolic phosphoglycerate kinase 2 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                           20.7%; Score 58.5; DB 10; Length 612; 38.3%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
EMBL. AB01841; BAA33802.1; -.
InterPro; IPR001576; PGK.
Pfam; PF00162; PGK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.5%; Score 58; DB 10; Length 401; 29.5%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lombardy poplar.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP
PHOSPHO-D-GLYCEROYL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative 11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                    1 MRRCVRHVLGIGLIVLKNLYFHKNSM---YPSP--KLSSFQEAFLFF 42
                                                                                                                                                                                                                                                                                           612 AA; 66380 MW; 9BE54BBB4242A91F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycolysis; Kinase; Transferase.
SEQUENCE 401 AA; 42669 MW; 79B095EE6B1A9DA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRRCVRHVLGIGLIVLKNLYFHKNSMYPSP----KLSSFQEAFL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Phosphoglycerate kinase (EC 2.7.2.3).
                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 AA.
                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0477; PHGLYCKINASE, PROSITE; PS00111; PGLYCERATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                      MEDLINE=97432142; PubMed=9286106;
                                                           Science 270:1804-1806(1995).
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
                                                                                                          STRAIN=IRBB21;
                                                                                                                                                                                                                                                                                                                           Query ...
Best Local Similar
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                         Query Match
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RESULT 7

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INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                         Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Epidendroideae; hygher Epidendroideae; Maxillarieae; Zygopetalinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams N.H., Chase M.W., Fulcher T., Whitten M.W.; "Molecular systematics of the Oncidiinae based on evidence from four DNA sequence regions: expanded circumscriptions of Cyrtochilum, Erycina, Otoglossum, and Trichocentrum, and a new genus (Orchidaceae).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Epidendroideae; Aygopetalinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Mismatches 13; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LIVLKNLYFHKNSMYPS------PKLSSFQEAFL-FFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lindleyana 16:113-139(2001).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.5%; Score 58; DB 8; Length 440; 29.6%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AA; 52685 MW; CFFBAF87755FF9E5 CRC64;
                                          (TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                   Probable intron maturase (Maturase K) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probable intron maturase (Maturase K) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00436; PEROXIDASE_2; UNKNOWN_1. Chloroplast; mRNA processing.
                                                                                                                                                                                                                                                                                                                                                              EMBL; AF239415; AAK31812.1; -
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
InterPro; IPR002016; Peroxidase.
                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seg
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Conservative
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pescatorea lehmannii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                        NCBI_TaxID=125110;
                                                                                                  Dichaea muricata.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=125160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440
                                                       01-MAR-2002
                                                                                                                Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pescatorea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
             Q9BB39;
09BB39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q95BP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q95BP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q95BP4
            g
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09BB33;

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"Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with special emphasis on Stanhopeinnes Combined molecular evidence."; submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
|- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTRONS (BY SIMILARITY)
-1-SMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASIS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS
-i- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Epidendroideae; higher Epidendroideae; Zygopetalinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 LIVLKNLYFHKNSMYPS------PKLSSFQEAFL-FFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                     269 LILMKKWKFHLVNFWQSYFHFWFQPYRIHIKKLPNYSFSFLGYFSIVLKNPLVV 322
                                                                                                                                                                                                                                                                                    13 LIVLKNLYFHKNSMYPS-------FKLSSFQEAFL-FFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.5%; Score 58; DB 8; Length 452; 29.6%; Pred. No. 20; tive 11; Mismatches 13; Indels
                                                                                                                                                                                                                    DB 8; Length 446;
                                                                                                                                                                                                                                                     13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452 AA; 53955 MW; A978F3CF6B10BA25 CRC64;
                                                                                                                                                                                     446 AA; 53294 MW; BC07C941362FBB6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
                                                                                                                                                                                                                                                     11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    452 AA
                                                                                                                                                                                                                    Score 58; DB Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF239422; AAK31819.1; -.
Interpro; IPR000005; HTHAraC.
Interpro; IPR000442; Intron_maturse2.
                                              EMBL; AF350662; ARK77125.1; -.
Interpro; IPR000442; Intron_maturse2.
Interpro; IPR002866; Matk.N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast; mRNA processing.
                                                                                                                                        Chloroplast; mRNA processing.
                                                                                                                                                                                                                       20.5%;
29.6%;
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                                                                                                                                                                                                                                                        16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             452
                                                                                                                                                                          446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pescatorea lehmannii.
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=125160;
                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pescatorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
NON_TER
SEQUENCE
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                                                                                                                                                                                                                           Query Match
                                                                                                                                                         NON_TER
NON_TER
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                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                        Q9BB32
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Whitten M., Williams N.H., Chase M.W.; Whitten M., Williams N.H., Chase M.W.; Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with special emphasis on Stanhopeinae: Combined molecular evidence."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whitten M., Williams N.H., Chase M.W.;
Whitten M., Williams N.H., Chase M.W.;
Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with
special emphasis on Stanhopeinae: Combined Michecular evidence.";
Submitted (FEB-2000) to the EMBL/GEDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epidendroideae; higher Epidendroideae; Maxillarieae; Zygopetalinae;
                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Asparagales, Orchidaceae, Epidendroideae, higher Epidendroideae, Maxillarleae, Zygopetallnae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 LILMKKWKFHLVNFWQSYFHFWFQPYRIHIKKLPNYSFSFLGYFSIVLKNPLVV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 LIVLKNLYFHKNSMYPS------PKLSSFQEAFL-FFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 8; Length 457;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 AA; 54601 MW; 06B18D9267078E9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probable intron maturase (Maturase K) (Fragment).
                                                              Probable intron maturase (Maturase K) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF239421; AAK31818.1; -.
InterPro; IPR000005; HTHATAC.
InterPro; IPR00442; Intron_maturse2.
InterPro; IPR002866; MatK.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Přam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF239416; AAK31813.1; -.
                                                                                                  Chondrorhyncha reichenbachiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast; mRNA processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=125111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                          NCBI_TaxID=125095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dichaea neglecta.
                                                                                                                                                                                                                                             SECUENCE FROM N.A
                                                                                                                                                                                            Chondrorhyncha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast
                                                                                                                          Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
NON_TER
SEQUENCE
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                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Felleisen R.S., Gottstein B.;
"Comparative analysis of full-length antigen II/3 from Echinococcus multilocularis and E.granulosus.";
Parasitology 109:223-232(1994).
EMBL; U05574; AAA50581.1;
InterPro: IPR000299; Band_4.1.
InterPro: IPR00799; Ez/rad/moesin.
Pfam; PF00773; Band_41: 1.
                                                                                                                                          14;
                                                                                                                                                                         13 LIVLKNLYFHKNSMYPS------PKLSSFQEAFL-FFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 IGFPWSVIRNLSFHDKKFIIKPADKSAKE---FFFLVEKSKINKRILALCT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 LGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNP-----LTLCS 54
                                                                                                                 20.5%; Score 58; DB 8; Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 20.5%; Score 58; DB 5; Length 559; Local Similarity 33.3%; Pred. No. 25; length 559; les 17; Conservative 7; Mismatches 19; Indels
                                                                                                                                         13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECUOA_0310.
Encephalitozoon cuniculi.
Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
Cyclophyllidea; Taeniidae; Echinococcus.
NCBI_TaxID=6210;
                                                                                             486 AA; 58096 MW; EAB0B4C50058B5CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS, PRO0935, BAND41.
SMART; SM00295, B41; 1.
PROSITE; PS50057; BAND_41_3; 1.
SEQUENCE 559 Aa; 65213 MW; 4781F013BAD92DA5 CRC64;
                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
265 proteasome regulatory subunit 4.
                                                                                                                                       11; Mismatches
                                                                                                                                                                                                                                       559 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 795 AA
          InterPro; IPR002866; Matk.N.
InterPro; IPR002016; Peroxidase.
Pfam; PP01348; Intron_maturas2; 1.
Pfam; PF01824; Matk.N; 1.
PROSITE; PS00436; PEROXIDASE_2; UNKNOWN_1.
                                                                                                                               Pred. No. 22;
InterPro; IPR000442; Intron_maturse2
                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94366818; PubMed=7521956;
                                                                                                                            Best_Local Similarity 29.6%;
Matches 16; Conservative 1
                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                     Echinococcus granulosus
                                                                                    486
                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CATTLE ISOLATE;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                   486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6035;
                                                                                                                                                                                                                                                                                           Antiqen II/3.
                                                                                   NON_TER
SEQUENCE
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       088865;
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                                                                             MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prantice M.B., Sebathia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Leatherl T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leathers S., Oyston P.C.F., Quail M., Rutherford K.,
"Genome sequence of Yersinia pestis, the causative agent of plague.";
Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQ-----EAFLFFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671 LGKGLLSISPLYFDKTTFMPKNTIGLFSTVFMLLDSSISPLVSS--HAYMFFLL 722
                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                           9 LGIGLIVLKNLYFHKNSMYP-------SPKLSSFQEAFLFFFL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58; DB 5; Length 795;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches 11; Indels
                    Genoscope;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome 413:523-527(2001).
Nature 413:523-527(2001).
EMBL: A.414145; CAC89775.1; -.
Interpro; IPR000130; Zn_MTpeptdse.
PROSITE; PS00142; ZINC_ENERS, UNKNOWN_1.
PROSITE; PS00142; ZINC_ENERS, UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein YP00932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 AA
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                                                                                                                                                                                                                                                                                                                                                  31.5%;
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                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=632;
STRAIN-GB-M1;
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Q8ZHG6
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Q9BB34
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RN SEQUENCE FROM N.A. (Chase M.W.)

REPORTED TO STATE TO STATE TO STATE THE SEQUENCE FROM N.A. (Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with whitten M., Williams N.H., Chase M.W.)

Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with state of State 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 20.1%; Score 57; DB 8; Length 503; Local Similarity 29.6%; Pred. No. 30; los 16; Conservative 11; Mismatches 13; Indels 14; Gaps
                                                                                                                                            Chloroplast.

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Asparagales; Orchidaceae;
Spermatophyta; Migher Epidendroideae; Maxillarieae; Zygopetalinae;
Cryptarrhena.

NCBL_TaxID-125104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 LIVLKNLYFHKNSMYPS------PKLSSFQEAFL-FFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503 503
503 AA; 60144 MW; C9C114E8B9A03000 CRC64;
01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Probable intron maturase (Maturase K) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: November 21, 2002, 13:42:27 Job time : 33 secs
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1 MRRCVRHVLGIGLIVLKNLY......FOEAFLFFFLILKNPLTLCS 54
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1: \cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*

2: \cgn2_6/ptodata/1/paa/USO6_COMB.pep:*

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                         OM protein - protein search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Sequence 164, App Sequence 218, App Sequence 4675, Ap Sequence 5353, Ap Sequence 5353, Ap Sequence 5353, Ap Sequence 29013, A Sequence 30438, Ap Sequence 30438, Ap Sequence 30438, Ap Sequence 30438, Ap Sequence 25795, Ap Sequence 59523, A Sequence 59522, A Sequenc
                                                                                                                                                                                                            Sequence 20013, A Sequence 3043, A Sequence 3043, A Sequence 30437, A Sequence 30437, A Sequence 3552, A Sequence 59523, A Sequence 59523, A Sequence 59521, A Sequence 2457, A Sequence 3521, A 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 58, Appl
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Sequence 38
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Best Local Similarity 100.0%; Pred. No. 1.4e-27;
Matches 54; Conservative 0; Mismatches 0; Indels
                                                                                                                          US-09-764-891-5555
US-09-764-891-5555
US-09-764-891-5553
US-09-708-427-29014
US-09-708-427-29013
US-09-935-625-9686
US-09-935-625-9686
US-09-935-625-30437
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US-09-771-288-38
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SERERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 64 Human Secreted Proteins
FILE REFERENCE: P2011PCT
CURRENT APPLICATION NUMBER: PCT/US98/14613
CURRENT FILING DATE: 1998-07-15
EARLIER FILING DATE: 1997-07-16
NUMBER OF SED ID NOS: 178
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                CT-US98-14613-142
 PCT-US98-14613-142
SEQ ID NO 142
LENGTH: 54
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RESULT

Sequence 142, App Sequence 142, App Sequence 142, App Sequence 6555, Ap Sequence 6555, Ap

PCT-US98-14613-142 0 US-09-229-982-142 0 US-09-688-142 1 US-09-776-724A-142 PCT-US01-01334-6555 US-09-764-874-6555

> 100.0 100.0 100.0 25.8 25.8

Sequence 142, App

Description

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Query Match Length

Score

Result

100.0

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FILE REFERENCE: PZ011P1
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US-09-776-724A-142
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LENGTH: 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; APPLICANT: Rosen et al. ; TITLE OF INVENTION: 64 Human Secreted Proteins
                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: 64 Human Secreted Proteins
                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/229,982
CURRENT APPLICATION NUMBER: US/09/229,982
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 1998-07-15
EARLIER PELICATION NUMBER: 1997-07-16
EARLIER FILING DATE: 60/052,861
EARLIER FILING DATE: 60/052,872
EARLIER PPLICATION NUMBER: 1997-07-16
EARLIER PPLICATION NUMBER: 1997-07-16
EARLIER PPLICATION NUMBER: 1997-07-16
EARLIER FILING DATE: 60/052,874
EARLIER PPLICATION NUMBER: 1997-07-16
EARLIER APPLICATION NUMBER: 1997-07-16
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EARLIER APPLICATION NUMBER: 1997-07-16
EARLIER PILING DATE: 60/052,873
EARLIER PILING DATE: 60/052,875
EARLIER PILING DATE: 60/053,440
EARLIER PILING DATE: 60/053,440
EARLIER PILING DATE: 60/053,440
EARLIER PILING DATE: 60/053,441
EARLIER FILING DATE: 60/053,442
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EARLIER PELLING DATE: 00/053,441
EARLIER PELLING DATE: 60/053,441
EARLIER APPLICATION NUMBER: 1997-07-22
EARLIER FILING DATE: 60/053,442
EARLIER FILING DATE: 60/056,359
EARLIER FILING DATE: 60/056,359
EARLIER FILING DATE: 60/056,359
EARLIER FILING DATE: 60/056,397
EARLIER FILING DATE: 60/055,725
EARLIER APPLICATION NUMBER: 1997-08-18
EARLIER FILING DATE: 60/055,985
EARLIER FILING DATE: 60/055,985
EARLIER FILING DATE: 60/055,987
EARLIER FILING DATE: 60/055,987
EARLIER FILING DATE: 60/055,987
EARLIER FILING DATE: 60/055,361
EARLIER APPLICATION NUMBER: 1997-08-18
EARLIER PILING DATE: 60/055,361
EARLIER PAPLICATION NUMBER: 1997-08-18
EARLIER PELING DATE: 60/055,726
EARLIER FILING DATE: 60/055,726
EARLIER FILING DATE: 60/055,726
EARLIER FILING DATE: 60/055,724
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EARLIER FILING DATE: 60/055,683
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 142, Application US/09669688
; GENERAL INFORMATION:
                                           Sequence 142, Application US/09229982 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                  FILE REFERENCE: PZ011P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-669-688-142
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100.0%; Pred. No. 1.4e-27;
tive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TTTLE OF INVENTION: 64 Human Secreted Proteins
FILE REFERENCE: PZ011
CURRENT APPLICATION NUMBER: US/09/776,724A
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/180,909
CURRENT APPLICATION NUMBER: US/09/669,688 CURRENT FILING DATE: 2000-09-26
                                                                              PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: PCT/US98/14613
PRIOR FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/053,441
PRIOR FILING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/053,442
PRIOR APPLICATION NUMBER: 60/056,359
PRIOR PAPLICATION NUMBER: 60/056,359
PRIOR PAPLICATION NUMBER: 60/055,725
PRIOR PILING DATE: 1997-08-18
PRIOR PILING DATE: 1997-08-18
PRIOR PILING DATE: 1997-08-18
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PRIOR PILING DATE: 1997-08-18
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PRIOR APPLICATION NUMBER: 60/052,874
PRIOR PILLING DATE: 1997-07-16
PRIOR APPLICATION NUMBER: 60/052,873
PRIOR PILLING DATE: 1997-07-16
PRIOR PELLING DATE: 1997-07-20
PRIOR FILLING DATE: 1997-07-20
PRIOR FILLING DATE: 1997-07-20
PRIOR FILLING DATE: 1997-07-20
PRIOR PELLING DATE: 1997-07-20
PRIOR PELLING DATE: 1997-07-20
PRIOR PELLING DATE: 1997-07-20
                                                         PRIOR APPLICATION NUMBER: US/09/229,982
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PRIOR APPLICATION NUMBER: 60/055,946
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PRIOR APPLICATION NUMBER: 60/055,683
NUMBER OF SEQ ID NOS: 294
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APPLICATION NUMBER: 60/053,440
FILING DATE: 1997-07-22
APPLICATION NUMBER: 60/053,441
                                                                                                                                              PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/052,661
PRIOR FILING DATE: 1997-07-16
PRIOR APPLICATION NUMBER: 60/052,872
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/19,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-18
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR PELING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR PILING DATE: 2000-08-14
PRIOR PELING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/226,447
PRIOR APPLICATION NUMBER: 60/226,868
PRIOR PELING DATE: 2000-08-14
PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/226,868
PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/226,369
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/224,518
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-29
PRIOR PILIN
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APPLICATION UNDBER: 60/251,868
FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/229,344
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PRIOR APPLICATION NUMBER: 60/234,997
PRIOR FILING DATE: 2000-09-01
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APPLICATION NUMBER: 60/229,343
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PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,345
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Best Local Similarity 100.0%; Score 283; DB 21; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.4e-27;
Matches 54; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCIOLOCT
CURRENT APPLICATION NUMBER: PCT/US01/01334
CURRENT FILING DATE: 2001-01-17
OR FILING DATE: 2000-02-08
OR APPLICATION NUMBER: 09/669,688
OR PILING DATE: 2000-09-26
OR FILING DATE: 1909-01-14
OR FILING DATE: 1999-01-14
OR FILING DATE: 1998-07-15
OR FILING DATE: 1998-07-15
OR APPLICATION NUMBER: 60/052,661
OR APPLICATION NUMBER: 60/052,871
OR FILING DATE: 1997-07-16
OR APPLICATION NUMBER: 60/052,872
OR FILING DATE: 1997-07-16
OR APPLICATION NUMBER: 60/052,871
OR APPLICATION NUMBER: 60/052,874
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OR PILING DATE: 1997-07-16
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OR APPLICATION NUMBER: 60/052,873
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OR FILING DATE: 1997-07-16
                                                                                                                          PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR PELICATION NUMBER: 09/229,982
PRIOR PELING DATE: 1998-07-15
PRIOR PELING DATE: 1998-07-15
PRIOR PAPLICATION NUMBER: 60/052,661
PRIOR PELING DATE: 1997-07-16
PRIOR APPLICATION NUMBER: 60/052,872
PRIOR PELING DATE: 1997-07-16
PRIOR APPLICATION NUMBER: 60/052,874
PRIOR APPLICATION NUMBER: 60/052,874
PRIOR PELING DATE: 1997-07-16
PRIOR PELING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/053,442
PRIOR PELING DATE: 1997-07-22
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PRIOR APPLICATION UNBER: 60/055,725
PRIOR APPLICATION NUBER: 60/055,985
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,985
PRIOR FILING DATE: 1997-08-18
PRIOR PILING DATE: 1997-08-18
PRIOR PILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,361
PRIOR APPLICATION NUMBER: 60/055,726
PRIOR PILING DATE: 1997-08-18
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PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,946
PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,683
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 294
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SEQ ID NO 142
LENGTH: 54
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PRIOR RELIUNG DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/29,513
PRIOR PELLAGATION NUMBER: 60/29,513
PRIOR PELLAGATION NUMBER: 60/23,413
PRIOR PELLAGATION NUMBER: 60/234,413
PRIOR PELLAGATION NUMBER: 60/234,413
PRIOR PELLAGATION NUMBER: 60/235,509
PRIOR PELLING DATE: 2000-09-05
PRIOR PELLING DATE: 2000-09-05
PRIOR PELLING DATE: 2000-09-29
PRIOR PELLING DATE: 2000-09-29
PRIOR PELLING DATE: 2000-09-29
PRIOR PELLING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/235,300
PRIOR PELLING DATE: 2000-10-02
PRIOR PELLING DATE: 2000-11-03
PRIOR PELLING DATE: 2000-11-03
PRIOR PELLING DATE: 2000-10-02
PRIOR PELLING DATE: 2000-11-03
PRIOR PELLING DATE: 2000-10-02
PRIOR PELLING DATE: 2000-10-02
PRIOR PELLING DATE: 2000-10-02
PRIOR PELLING DATE: 2000-10-03
PRIOR PELLING DATE: 2000-10-13
PRIOR PELLING DATE: 2000-11-17
PRIOR PELLING DATE: 200
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1 MRRC-----VRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLTLC 53
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                                                                                    PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,264
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR PELLING DATE: 2000-11-17
PRIOR PELLING DATE: 2000-11-17
PRIOR PELLING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-18
PRIOR PELLING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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APPLICATION NUMBER: 60/233,065
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                             FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,215
APPLICATION NUMBER: 60/249,211
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Matches 18; Conservative
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R APPLICATION NUMBER: 60/220,963
R FILING DATE: 2000-07-26
R APPLICATION NUMBER: 60/217,496
R FILING DATE: 2000-07-11
R APPLICATION NUMBER: 60/225,447
R FILING DATE: 2000-08-14
R FILING DATE: 2000-08-14
R FILING DATE: 2000-07-14
R FILING DATE: 2000-07-14
R FILING DATE: 2000-07-14
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R APPLICATION NUMBER: 60/225,267

R APPLICATION NUMBER: 60/225,267

R APPLICATION NUMBER: 60/216,880

R FILING DATE: 2000-09-14

R APPLICATION NUMBER: 60/225,270

R APPLICATION NUMBER: 60/225,270

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R APPLICATION NUMBER: 60/225,370

R FILING DATE: 2000-12-08

R FILING DATE: 2000-12-08

R FILING DATE: 2000-9-27

R APPLICATION NUMBER: 60/234,274

R FILING DATE: 2000-09-27 NR APPLICATION NUMBER: 60/234,223

PR FILING DATE: 2000-09-21

PR APPLICATION NUMBER: 60/228,924

PR FILING DATE: 2000-08-30

PR FILING DATE: 2000-08-30

PR FILING DATE: 2000-08-14

PR FILING DATE: 2000-08-14

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PR FILING DATE: 2000-08-18

PR FILING DATE: 2000-08-18

PR FILING DATE: 2000-08-18

PR FILING DATE: 2000-08-18

PR FILING DATE: 2000-08-18 PRIOR PAPLICATION NUMBER: 60/251,868
PRIOR PAPLICATION NUMBER: 60/251,856
PRIOR PLING DATE: 2000-12-08
PRIOR FILING DATE: 7000-12-08
PRIOR FILING DATE: 7000 APPLICATION NUMBER: 60/225,758 FILING DATE: 2000-08-14 FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/244,617
FILING DATE: 2000-11-01
APPLICATION NUMBER: 60/225,268 APPLICATION NUMBER: 60/229,343
APPLICATION NUMBER: 60/229,343 FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,513
FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/231,413
FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/226,868 FILING DATE: 2000-08-22 APPLICATION NUMBER: 60/216,647 FILING DATE: 2000-07-07 FILING DATE: 2000-07-26
APPLICATION NUMBER: 60/241,809
FILING DATE: 2000-10-20 FILING DATE: 2000-12-08 APPLICATION NUMBER: 60/229,344 APPLICATION NUMBER: 60/229,345 FILING DATE: 2000-09-01 APPLICATION NUMBER: 60/229,287 APPLICATION NUMBER: 60/220,964 FILING DATE: 2000-07-26 APPLICATION NUMBER: 60/249,299 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/236,327 FILING DATE: 2000-09-29 APPLICATION NUMBER: 60/241,785 FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/236,368 PRIOR FILING DATE: 2000-09-01 PRIOR APPLICATION NUMBER: 60/234,997 PRIOR
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PRIOR APPLICATION NUMBER: 60/236, 567
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-23
PRIOR FILING DATE: 2000-00-23
PRIOR PAPLICATION WINBER: 60/237, 039
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION WINBER: 60/236, 802
PRIOR APPLICATION WINBER: 60/236, 802
PRIOR APPLICATION WINBER: 60/236, 802
PRIOR PILING DATE: 2000-10-02
PRIOR APPLICATION WINBER: 60/236, 935
PRIOR PILING DATE: 2000-10-02
PRIOR PLING DATE: 2000-10-02
PRIOR PILING DATE: 2000-10-13
PRIOR APPLICATION WINBER: 60/239, 935
PRIOR PILING DATE: 2000-10-13
PRIOR APPLICATION WINBER: 60/239, 935
PRIOR PILING DATE: 2000-10-13
PRIOR APPLICATION WINBER: 60/246, 747
PRIOR APPLICATION WINBER: 60/246, 747
PRIOR APPLICATION WINBER: 60/246, 747
PRIOR APPLICATION WINBER: 60/249, 216
PRIOR PILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-11-17
PRIOR APPLICATION WINBER: 60/225, 214
PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000

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PRIOR APPLICATION NUMBER: 09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
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PRIOR FILING DATE: 1998-03-06
PRIOR PEDLICATION UNBER: 60/040,162
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR APPLICATION NUMBER: 60/038,621
PRIOR FILING DATE: 1997-03-07
PRIOR FILING DATE: 1997-03-07
PRIOR FILING DATE: 1997-03-07
PRIOR PELICATION NUMBER: 60/038,621
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R APPLICATION NUMBER: 60/047, 502

R APPLICATION NUMBER: 60/047, 633

R APPLICATION NUMBER: 60/047, 633

R FILING DATE: 1997-05-23

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R APPLICATION NUMBER: 60/047, 583
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APPLICATION UNMBER: 60/047,598
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,600
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APPLICATION UNMBER: 60/047,618
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/047,584
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,582
FILING DATE: 1997-05-23
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PRIOR APPLICATION NUMBER: 09/809,391
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APPLICATION NUMBER: 60/040,334
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APPLICATION NUMBER: 60/040,336
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APPLICATION NUMBER: 60/047,597
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APPLICATION NUMBER: 60/047,592
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APPLICATION NUMBER: 60/047,581
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APPLICATION NUMBER: 60/047,587
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                         21; Conservative
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         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.8%; Score 73; DB 21; Length 85; Best Local Similarity 30.5%; Pred. No. 0.67; Matches 18; Conservative 11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 362, Application US/09809391
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REPERENCE: P200029
CURRENT APPLICATION UNMER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
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R FILING DATE: 2000-10-20
R FILING DATE: 2000-11-08
R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/231, 243
R R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/233, 065
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R PRILING DATE: 2000-09-08
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R APPLICATION NUMBER: 60/241,808
R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/241,826
R FILING DATE: 2000-10-20
R FILING DATE: 2000-10-20
R FILING DATE: 2000-10-20
         FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,297
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/232,400
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FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/232,081
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APPLICATION NUMBER: 60/232,080
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APPLICATION NUMBER: 60/232,399
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APPLICATION NUMBER: 60/232,401
                                                                                   FILING DATE: 2000-09-14
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LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (132)
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Query Match

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17; Gaps
                                           1 MRRCVRH-VLGIGLIVLKNLYFHKNSMYPS-----PKLSSFQEAFL-FFFLIL 46
                                                                    9; Indels
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
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R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,314
R APPLICATION NUMBER: 60/043,569
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,311
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/056,877
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,889
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,893
R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,630
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R APPLICATION NUMBER: 60/056,894
R PILING DATE: 1997-08-22
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R APPLICATION NUMBER: 60/056,911
R FILING DATE: 1997-08-22 PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,612
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,632 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,669
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 APPLICATION NUMBER: 60/047,596 APPLICATION NUMBER: 60/047,601 FILING DATE: 1997-05-23 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 1997-05-23 FILING DATE: 1997-04-1 FILING DATE:

PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,631
PRIOR APPLICATION NUMBER: 60/056,845
PRIOR PILING DATE: 1997-08-22
PRIOR PAPLICATION NUMBER: 60/056,892
PRIOR PILING DATE: 1997-08-22
PRIOR PILING DATE: 1997-08-22
PRIOR PILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,599
PRIOR PILING DATE: 1997-05-23
PRIOR PELING DATE: 1997-06-23
PRIOR PELING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 60/047,501
PRIOR PELING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 60/043,576
PRIOR APPLICATION NUMBER: 60/043,576
PRIOR PELING DATE: 1997-06-23 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,875 APPLICATION NUMBER: 60/056,908 FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: 60/057,669 PRIOR FILLING DATE: 1997-09-05 PRIOR APPLICATION NUMBER: 60/049,610 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 APPLICATION NUMBER: 60/056,909 APPLICATION NUMBER: 60/056,862 APPLICATION NUMBER: 60/056,887 PRIOR APPLICATION NUMBER: 60/048,964 PRIOR FILING DATE: 1997-06-06 PRIOR APPLICATION NUMBER: 60/057,650 PRIOR APPLICATION NUMBER: 60/056,884 PRIOR FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 PRIOR FILING DATE: 1997-09-05 997-08-22 FILING DATE: 1997-08-2 997-08-2 FILING DATE: FILING DATE: PRIOR FILING DATE: PRIOR

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Indels 17; Gaps

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Ouery Match 22.8%; Score 64.5; DB 22; Length 132; Best Local Similarity 37.5%; Pred. No. 12; Matches 21; Conservative 9; Mismatches 9; Indels 17;

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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
CURRENT APPLICATION NUMBER: PCT/US01/01330
CURRENT FILING DATE: 2001-01-13
CURRENT FILING DATE: 2001-01-13
PLICE APPLICATION data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 437
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA119PCT
CURRENT APPLICATION NUMBER: PCT/US01/01330
CURRENT FILING DATE: 2001-01-13
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 437
SOFTWARE: Patentin Ver. 2.0
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                                                                                      PAPLICATE: ROSen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-09-08
NUMBER OF SEQ ID NOS: 757
SOFTWARE: PATENTIN PATENTION NUMBER: PCT/US98/04493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (132)
; OTHER INFORMATION: Xaa equals stop translation
US-10-164-861-362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.8%; Score 64.5; Di
37.5%; Pred. No. 12;
tive 9; Mismatches
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                                         ; Sequence 362, Application US/10164861; GENERAL INFORMATION:
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13 LIVLKSFFFFKDSLTPSPRL 32
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Matches 21; Conservative
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PCT-US01-01330-164
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PCT-US01-01330-218
                       US-10-164-861-362
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RESULT 9
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Sequence 5353, Application PC/TUSO101339
Sequence 5353, Application PC/TUSO101339
GENERAL INFORMATION:
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILLE REFERENCE: PC006PCT
CURRENT APPLICATION NUMBER: PCT/USO1/01339
CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SEQ ID NO 5353
                                                                                                                                                                                                                                                                                                                                          PCT-US01-01339-4675

Sequence 4675, Application PC/TUS0101339

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006PCT
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                                                                                                                                  22.6%; Score 64; DB 1; Length 89; 60.0%; Pred. No. 9.6;
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CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4675
LENGTH: 89
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APPLICANT: Rosen et al.
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13 LIVLKSFFFFKDSLTPSPRL 32
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Best Local Similarity 60.03
Matches 12; Conservative
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Matches 12; Conservative
SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 218 LENGTH: 89
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PCT-US01-01339-5353
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pcr-us01-01330-218
                                                                                                                                                             Best Local Similarity
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US-09-764-891-4675
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US-09-764-891-5353
is Sequence 5353, Application US/09764891
s GENERAL INFORMATION:
i APPLICAMT: Rosen et al.
i TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
i TITLE OF INVENTION: NUCLEIC ACIDS, Proteins, and Antibodies
i TITLE REFERENCE: PC006
i CURRENT APPLICATION UNBER: US/09/764,891
cURRENT FILING DATE: 2001-01-17
i Prior application data removed - consult PALM or file wrapper;
i NUMBER OF SEQ ID NOS: 10231
i SOFTWARE: Patentin Ver. 2.0
i SEQ ID NO 5353
i LENGTH: 89
i TYPE: PRT
i ORGANISM: Homo sapiens
US-09-764-891-5353
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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PC006
CURRENT APPLICATION NUCLE: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper. NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4675
LENGTH: 89
TYPE: PRT
TYPE: PRT
CORGANISM: Homo sapiens
US-09-764-891-4675
                                                                                                                                                                                                                                                                                                                                                            Query Match 22.6%; Score 64; DB 21; Length 89; Best Local Similarity 60.0%; Pred. No. 9.6; Matches 12; Conservative 5; Mismatches 3; Indels
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13 LIVLKSFFFFKDSLTPSPRL 32
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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: November 21, 2002, 13:41:56; Search time 10 Seconds

(without alignments)

186.011 Million cell updates/sec

Title: US-09-776-724A-142

Perfect score: 283
Sequence: 1 MRRCVRHVLGIGLIVLKNLY.......FQEAFLFFFLILKNPLTLCS 54

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 99223 segs, 34446456 residues

Total number of hits satisfying chosen parameters: 99223

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Maximum Match 100%
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Se : Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US00_NEW_COMB.pep:*

Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	! .	1435,	Sequence 69043, A	190. A	512,		512,	512,		512,	512,		512,	512,		512,	512,	512,	512,	512,	512,		512,		512,	512,
SUMMARIES		US-10-092-411A-4480	10-264-237-143	19-724-676-69	0-230	10-131-813A-	-131-	10-131-823A-	10-131	10-131-826A-	0-131	.0-125-	10-127-	US-10-127-831A-512	.127-835A-	337A-	US-10-127-842A-512	\cdot 12		.128-689A-	0-131-	US-10-131-833A-512	0 - 131 -	0-125-	0-127-	-10-127-838B-	US-10-127-843A-512
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Sequence 1435, Application US/10264237
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-19

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222222333333222222	ALIGNMENTS /10092411A mm et al ACID AND AMINO IDIS FOR DIAGNO US/10/092,411A 3-07 60/064,964 60/055,779 4 idermidis	CZE H I
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716 716 716 716 716 716 716 716 716 716	SULT 1 -10-092-411A-4480 Sequence 4480, Application US/10092411 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION: EPIDERMIDIS FOR FITLE REFERENCE: 032796-101 CURRENT APPLICATION NUMBER: US/10/092 CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,9 PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1997-11-08 PRIOR FILING SEQ ID NOS: 5676 LENGTH: 673 TYPE: PRT ORGANISM: Staphylococcus epidermidis -10-092-411A-4480	tch 20.7%; Score al Similarity 32.3%; Pred 20; Conservative 7; Mis RHVLGIGLIVLKNLYF :: : : : : : :
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8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4480 ATADO ATADO NATION NATION ATION ATION TATON TATON ATION ATION ABO	Similarity 0; Conserv L iVPFISVISIL 48
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	ULT 1 10.092-411A-4480 equence 4480, Application experience 4480, Application aPPLICANT: Lynn Doucette-S TITLE OF INVENTION: BIDE FILE REFERENCE: 032796-101 CURRENT APPLICATION NUMBER CURRENT APPLICATION NUMBER: PRIOR PILING DATE: 1998-08 PRIOR FILING DATE: 1998-08 PRIOR FILING DATE: 1997-08 PRIOR FILING DATE: 1997-08 PRIOR FILING DATE: 1997-08 FRIOR FILING DATE: 1997-11	Match Socal Simil. Socal Simil. Socal Simil. RHILYPEII. I RHIIVPEII. 7 KN 48 9 AN 80
27. 27. 27. 27. 27. 27. 27. 27. 27. 27.	ESULT 1 S-10.092-411A Sequence 448 GENERAL INFO APPLICANT: TITLE OF IN PRIOR FILLIN PRIOR FILLIN PRIOR FILLIN PRIOR FILLIN PRIOR FILLIN NUMBER OF S SEQ ID NO 44 TYPE: PRI TYPE: PRI ORGANISM: S-10-092-411A	y Ma Loc hes 6 21 47 79
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US-10-230-437-190
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                                                                                                                                                                                             ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-237-1435
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APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Collin L.
APPLICANT: Watanabe, Collin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLG94
CURRENT APPLICATION NUMBER: U5/10/30,437
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 69043, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 69043
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                                                                                                                                                                                                                                                                                                                                    14; Conservative
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Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: Patentin Ver. 3.1
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                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                    NAME/KEY: MISC_FEATURE
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US-09-724-676-69043
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US-10-230-437-190
                                            SEQ ID NO 1435
LENGTH: 172
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                                                                                              TYPE: PRT
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PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-12-17
PRIOR PLICATION NUMBER: 60/078910
PRIOR PLICATION NUMBER: 60/079294
PRIOR PLICATION NUMBER: 60/079294
PRIOR PLICATION NUMBER: 60/079294
PRIOR PLICATION NUMBER: 60/079265
PRIOR PAPLICATION NUMBER: 60/079656
PRIOR PAPLICATION NUMBER: 60/079656
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
SEQ ID NOS: 246
SEQ ID NOS: 246
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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CURRENT APPLICATION NUMBER: US/10/131,813A
PRIOR ADDITOTOTON NUMBER: US/10/131,813A
PRIOR ADDITOTOTOR
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PRIOR APPLICATION NUMBER: 60/04911

PRIOR FILING DATE: 1997-06-18

PRIOR PELLING DATE: 1997-06-18

PRIOR PELLING DATE: 1997-08-26

PRIOR FILING DATE: 1997-08-26

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17
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APPLICATION NUMBER: 60/059263
FILING DATE: 1997-09-18
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APPLICATION NUMBER: 60/059122
APPLICATION NUMBER: 60/059184
APPLICATION NUMBER: 60/059184
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Matches 13; Conservative
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Gurney, Austin L.
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Filvaroff, Ellen
Gao, Wei-Qiang
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ORGANISM: Homo Sapien
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Gaps

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17; Indels

336 VGLDSLESLSFYDNKLVKVPQLALQKVPNLKFLDLNKNPI 275

Dp

11 IGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50

Query Match
18.4%; Score 52; DB (Best Local Similarity 32.5%; Pred. No. 24; Matches 13; Conservative 10; Mismatches

US-10-131-819A-512

DB 6; Length 716;

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C134
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                  PRIOR FILING DATE: 1997-1997, PRIOR PRIOR APPLICATION WHRER: 60/059588
PRIOR FILING DATE: 1997-09-19
REMAINING PRIOR Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
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PRIOR PLILIG DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PLILIG DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PILING DATE: 1997-09-17
PRIOR PRILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-19
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PRIOR APPLICATION NUMBER: 60/059352
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PRIOR APPLICATION UNDBER: 60/049911
PRIOR FLING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
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Filvaroff, Ellen
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US-10-131-813A-512
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ORGANISM: Homo Sapien
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                                                                                                                                                  SEQ ID NO 512
LENGTH: 716
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LENGTH: 716
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CURRENT APPLICATION NUMBER: 05/049911

PRIOR PAPLICATION NUMBER: 05/049911

PRIOR PELING DATE: 1997-06-18

PRIOR PELING DATE: 1997-06-18

PRIOR PELING DATE: 1997-06-18

PRIOR PELING DATE: 1997-06-18

PRIOR PELING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/05912

PRIOR APPLICATION NUMBER: 60/05912

PRIOR APPLICATION NUMBER: 60/05912

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-19

PRIOR PELING DATE: 1997-09-19
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APPLICANT: Wood,William
APPLICANT: Wood,William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C143
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                           Sequence 512, Application US/10131823A
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Gurney, Austin L.
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Matches 13; Conserv
                                                    GENERAL INFORMATION:
US-10-131-823A-512
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LENGTH: 716
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETE BECODING THE SAME
FILE REFERENCE: P3330R1C126
FILE REFERENCE: P3330R1C126
FURRENT FILLING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
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PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056913
PRIOR FILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059127
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
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                                          Sequence 512, Application US/10131824A GENERAL INFORMATION:
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                      Gerritsen, Mary E.
Goddard, Audrey
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Best Local Similarity 32.58
Matches 13; Conservative
                                                                                      APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen
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Gurney, Austin L.
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Filvaroff, Ellen
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Filvaroff, Ellen
Gao, Wei-Qiang
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Smith, Victoria
                                                                                                                                     DeForge, Laura
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; ORGANISM: Homo Sapien
US-10-131-824A-512
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US-10-131-826A-512
RESULT 8
US-10-131-824A-512
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APPLICANT:
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PRIOR FILING NUMBER: 00/050974
PRIOR FILING DAME: 1997-08-26
PRIOR PELICATION NUMBER: 60/059113
PRIOR PELING DAME: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-19
PRIOR PELING DATE: 1997-09-19
PRIOR PILING DATE: 1997-09-19
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APPLICANT: Watenabe_Colin K
APPLICANT: Watenabe_Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERRORE: P3330F1C128
CURRENT APPLICATION NUMBER: 05/10/131,826A
CURRENT APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Stewart, Timothy A.
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Gerritsen, Mary E.
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Best Local Similarity 32.5%
Matches 13; Conservative
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                                  Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                      Sherwood, Steven
                                                                                                                                                        Smith, Victoria
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ORGANISM: Homo Sapien
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LENGTH: 716
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Smith, Victoria
Stewart, Timothy A.
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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ORGANISM: Homo Sapien
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LENGTH: 716
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                  APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C138
CURRENT APPLICATION NUMBER: US/10/131,829A
PRIOR APLICATION NUMBER: 60/04931
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-26
PRIOR FILING DATE: 1997-08-26
PRIOR PAPLICATION NUMBER: 60/056914
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PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059127
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PELLON NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059352
PRIOR RILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR PILING DATE: 1997-09-19
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Best Local Similarity 32.5%; Pred. No. 3
Matches 13; Conservative 10; Mismatch
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PRIOR APPLICATION NUMBER: 60/059115
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Wood, William
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APPLICANT: Beresini, Maureen
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Smith, Victoria
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Wood, William
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LENGTH: 716
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PRIOR FILING NAPEL 1997-09-17
PRIOR FILING NAPEL 1997-09-17
PRIOR PAPLICATION WINBER 06/059113
PRIOR FILING NAPEL 1997-09-17
PRIOR PAPLICATION WINBER 16/059115
PRIOR PAPLICATION WINBERS 16/059115
PRIOR PAPLICATION WINBERS 16/059114
PREPICATION PA
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11 IGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50
                        ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-127-831A-512
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C107
CURRENT APPLICATION NUMBER: US/10/127,831A
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                   PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR PLIING DATE: 1997-09-19
PRIOR PLIING DATE: 1997-09-19
PRIOR REPLICATION NUMBER: 60/059588
PRIOR PLIING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
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Best Local Similarity 32.5%; Pred. No. 24;
Matches 13; Conservative 10; Mismatches
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PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR PELING DATE: 1997-06-16
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PELING DATE: 1997-09-17
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PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PELING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-18
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PRIOR PELING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR PELING DATE: 1997-09-19
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PRIOR FILING DATE: 1997-09-17
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Gerritsen, Mary E.
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Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
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Filvaroff, Ellen
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SEQ ID NO 512
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US-10-127-829A-512
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                                                                                                                                                                                                                  SEQ ID NO 512
LENGTH: 716
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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NUMBER OF SEQ ID NOS: 550
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DB 6; Length 716; 24;
                                                        17; Indels
                                                                                                                                                             236 VGLDSLESLSFYDNKLVKVPQLALQKVPNLKFLDLNKNPI 275
                                                                                                                11 IGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50
  18.4%; Score 52; DB 6
32.5%; Pred. No. 24;
tive 10; Mismatches
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PRIOR APPLICATION NUMBER: 60/049911
PRIOR PLING DATE: 1997-06-18
PRIOR PLING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PAPLICATION NUMBER: 60/059115
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR PLING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059363
PRIOR PLING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059368
PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                    Sequence 512, Application US/10127835A GENERAL INFORMATION:
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Filvaroff, Ellen
Gao, Wei-Qiang
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Wood, William
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Query Match
Best Local Similarity 32.5%
Matches 13; Conservative
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Gurney, Austin L.
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ORGANISM: Homo Sapien
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APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C96

CURRENT APPLICATION NUMBER: US/10/127,837A

CURRENT FILING DATE: 1997-06-18

PRIOR FILING DATE: 1997-06-18

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-19

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236 VGLDSLESLSFYDNKLVKVPQLALQKVPNLKFLDLNKNPI 275
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                                                                                              RESULT 15
US-10-127-837A-512
Sequence 512, Application US/10127837A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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Watanabe, Colin K
Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Godowski, Paul J.
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ORGANISM: Homo Sapien
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LENGTH: 716
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GenCore version 5.1.3
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OM protein . protein search, using sw model

Run on:

(without alignments) 288.403 Million cell updates/sec November 21, 2002, 13:40:48; Search time 18 Seconds

US-09-776-724A-142 Perfect score;

1 MERCVRHVLGIGLIVLKNLY......FQEAFLFFFLILKNPLTLCS 54 Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		hypothetical prote	probable membrane	mannosyltransferas	hypothetical prote	protein kinase Xa2	conserved hypothet	probable membrane	tryptophan synthas	ORF MSV102 hypothe	hypothetical prote	G protein-coupled	Dranched-chain alp	ranched-chain	B. subtilis YbtB.p	B. subtilis YbtB p	hypothetical prote		hypothetical prote		hypothetical prote	glucans biosynthes	hypothetical prote	probable membrane	ADP,ATP carrier pr	aspartic proteinas	hypothetical prote	ubiquitin-protein	glutamine ABC tran NADH2 dehydrogenas
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	Score	63	09	09	58.5	58.5	57.5	56.5	56.5	26	26	26	26	26	26	26	26		n	'n	'n	55.5	'n	'n	4.	•	4.	4.	54	54
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	ENTS	Arabidopsis thaliana mouse-ear cress) ision 16-Ju1-1999 #text_c} neisen, A.; Wambutt, R.; E
B71802 E64715 S49788 T40065 T40065 C84078 S35380 F09709 F09709 F09728 T137390 C290089 JQ1896 F81319	ALIGNMENTS	RESULT 1 T09895 hypothetical protein T22A6.150 - Arabidopsis thai C.Speciales: Arabidopsis thaliana (mouse-ear cress) C.Bate: 16-Unl-1999 #sequence_revision 16-Jul-199 C.Accession: T09895 R.Bevan M.; Zimmermann, W.; Grueneisen, A.; Wamt
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588 633 633 780 1944 2971 230 332 346 644 744 1694 319		(2A6.150 thalian quence
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8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		RESULT 1 T09895 Cypecies Tablidopsis thaliana (Cybacces: Arabidopsis thaliana (Cybate: 16-701-1999 #sequence_rev Cyaccession: T09895 Rybevan, M.; Zimmernann, W.; Gruesubmitted to the property

Sep-2000		Gaps 1;
PRESULT 1709895 Hypothetical protein T22A6.150 - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000 R.Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; A.; Afference number: 216896	A: Molecule type: DNA A: Residues: 1-395 <bev> A: Residues: 1-395 <bev> A: Cross-references: EMBL: AL078637; GSPDB:GN00062; ATSP:T22A6.150 A: Experimental source: cultivar Columbia; BAC clone T22A6 C: Genetics: A: Aspension: 4 C: Superfamily: Arabidopsis thallana hypothetical protein T20010 100</bev></bev>	Query Match Best Local Similarity 33.3%; Score 63; DB 2; Length 395; Matches 17; Conservative 8; Mismatches 22; Indels 4; Qy 4 CVRHVLGIGLIVLKNIXFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50 :

probable membrane protein VGR069w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein G4554 C;Species: Saccharomyces cerevisiae C;Species: J7-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002 C;Accession: S64364 B:Wedler; H; Schaffe, M; Wedler, E; Wambutt, R. Submitted to the Protein Sequence Database, May 1996 A;Reference number: S64356

A Molecule type: DNA A; Residues: 1-111 <WED> A; Cross-references: EMBL:272853; NID:91323091; PID:91323093; GSPDB:GN00007; MIPS:YGR0 C;Genetics: A.Gene: MIPS.YGR069w A.Cross-references: SGD:S0003301 A.Map position: 7R C.Superfamily: Saccharomyces probable membrane protein YGR069w C.Keywords: transmembrane #status predicted <TMM>

Query Match

21.2%; Score 60; DB 2; Length 111;

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Gonserved hypothetical protein rP00932 [imported] - Yersinia pestis (strain C092) conserved hypothetical protein rP00932 [imported] - Yersinia pestis (strain C092) C. Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001 C. Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001 C. Date: 02-Nov-2001 #ren, Date: 03-Nov-2001 #ren, Date: 03-Nov-2001 R. W.; Date: 03-Nov-2001 R. W.; Date: 03-Nov-2001 R. W.; Date: 03-Nov-2001 R. Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, R.; Whitehead, S.; Barrel II, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, R.; Whitehead, S.; Barrel Nature 413, 523-527, 2001 Resina pestis, the causative agent of plague. A; Reference number: AB0001; MUID:21470413; PMID:11586360 A; Reference number: DNA A; Status: preliminary A; Molecule type: DNA A; Residues: 1-170 kWIR> A; Residues: 1-170 kWIR> A; Residues: 1-170 kWIR> A; Residues: 1-170 kWIR> A; Construction: 03-November: 03-Novem
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A;Nolecule type: DNA
A;Residucs: 1-612 <SON>
A;Cross-references: EMBL:U72726; NID:g2586078; PIDN:AAB82753.1; PID:g2586081
A;Experimental source: strain IRBB21
                              protein kinase Xa21 (EC 2.7.1.-) D, receptor type - long-staminate rice (Species: Oryza longistaminata (long-staminate rice) (S.Species: Oryza longistaminata (long-staminate rice) (C.Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 (S.Accession: T10727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Indels 13; Gaps
                                                                                                                                               R; Song, W.Y.; Pi, L.Y.; Wang, G.L.; Gardner, J.; Holsten, T.; Ronald, P.C. Plant Cell 9, 1279-1287, 1997
A; Title: Evolution of the rice xa21 disease resistance gene family. A; Reference number: 215276; MUID:97432142; PMID:9286106
A; Accession: T10727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.7%; Score 58.5; DB 2; Length 612; 38.3%; Pred. No. 14; tive 5; Mismatches 19; Indels
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A; Residues: 1-153 <VOE>
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Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: GB:AE000818; GB:AE000666; NID:92621384; PIDN:AAB84837.1; PID:9262138
A,Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Start codon: GTG
C;Superfamily: Methanobacterium thermoautotrophicum dolichyl-phosphate mannose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AF022980; PIDN:AAB69921.1; GSPDB:GN00023; CESP:T03D3.10
A;Experimental source: strain Bristol N2; clone T03D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T03D3.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                         mannosyltransferase - Methanobacterium thermoautotrophicum (strain Delta H) Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999 C;Accession: E69142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 RRAIRHILEEGLNYSGFELEAEMFSKLARAGLKIVEVPITYRKRS--DEPKLSSFTDGFK 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RRCVRHVLGIGL------39
                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD . 20 RHILVIGLELLSEVYLASKQTFYENKTRTQFMMLEDWIYLYL----PSTFCA 67
                          ;
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Local Similarity 30.8%; Pred. No. 9;
les 16; Conservative 11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.2%; Score 60; DB 2; Length 221; 30.9%; Pred. No. 3.2; tive 8; Mismatches 15; Indels
                              20; Indels
                                                                                              4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50
                                                                                                                                           C, Accession: T32214
R; Murray, J: Wohldmann, P.; Bauer, C.; Biewald, T.
R; Murray, J: Wohldmann, P.; Bauer, C.; Biewald, T.
Submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid T03D3.
A; Reference number: Z21136
A; Accession: T32214
A; Status: preliminary; translated from GB/EMBL/DDBJ
Best Local Similarity 34.0%; Pred. No. 1.5; Matches 16; Conservative 5; Mismatches
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A; Introns: 109/3; 235/3; 269/3; 326/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 30.99
nes 21; Conservative
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A; Residues: 1-394 <MUR>
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A; Residues: 1-221 <MTH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 LFFFLILK 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: E69142
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Rischweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T Genomics 23, 643-650, 1994
Ajrite. Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled recep A; Reference number: A55735; MUID:95154835; PMID:7851893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-321 <WIL>
A;Cross-references: EMBL:AL110500; NID:e1542314; PIDN:CAB54485.1; CESP:Y87G2A.k
                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-177 <ARO>
A;Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97649.1; PID:g4049689
C;Genetics: A;Note: MSV102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c; Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross_references: GB:L31580; NID:9468340; PIDN:AAA74232.1; PID:9468341 C; Superfamily: vertebrate rhodopsin C; Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.8%; Score 56; DB 2; Length 378; 32.6%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 32.4%; Pred. No. 15;
J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: 220484; MUID:99102612; PMID:9847359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Y87G2A.k - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, September 1999
                                                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB :
Pred. No. 8.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 29/1; 89/1; 189/1; 299/3
                                                                                                                                                                                                                                                                                                                                                                                                                   19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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A;Accession: T27463
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                                                                                                                  A; Accession: T28263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Pathway: tryptophan blosynthesis
A; Note: coffactor pyridoxal phosphate; last step in pathway
A; Note: coffactor pyridoxal phosphate beta chain; tryptophan synthase beta chain; tryptophan synthase beta chain; tryptophan synthase beta chain; tryptophan synthase beta chain; phosphoprotein; pyridoxal phosphate F; 4-386/Domain: tryptophan synthase beta chain homology <TRPB>
F; 4-386/Domain: tryptophan synthase beta chain homology <TRPB>
F; 85/Active site: His #status predicted
F; 86/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Munson, M.A.; Baumann, P.
J. Bacteriol. 175, 6426-6432, 1993
Afrittle: Molecular cloning and nucleotide sequence of a putative trpDC(F)BA operon in A; Reference number: A49897; MUID:94012512; PMID:8407819
A, Accession: C49897
       A; Cross-references: EMBL: Z73078; NID: g1323535; PID: e243264; PID: g1323536; MIPS: YGR293c
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C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T28263
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tryptophan synthase (EC 4.2.1.20) beta chain - Buchnera aphidicola
C;Species: Buchnera aphidicola
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Wolecule type: DNA*
A;Residues: 1-399 <MUN>
A;Cross.references: EMBL:219055; NID:9396655; PIDN:CAA79500.1; PID:9396658
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 7R
S.Superfamily: Saccharomyces cerevisiae probable membrane protein YGR293c
C;Keywords: transmembrane protein
P;6-22/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RCVRHV---LGIGLIVLKNLYFHKNSM-----YPSPKLSSFQEAFLFFFLILKNPLF 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORF MSV102 hypothetical protein - Melanoplus sanguinipes entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.0%; Score 56.5; DB 2; Length 1
27.0%; Pred. No. 6.1;
tive 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 IVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKN-----PLTLCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 ILMPALYQLEKNFVDAKKDSNFQKS---FFNYLKNYAGRPTPLTLCN 62
                                                                                      R;Watson, M.D. submitted to the Protein Sequence Database, May 1996 A;Reference number: S64630 A;Accession: S64630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.0%; Score 56.5; I
36.2%; Pred. No. 17;
                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-141 < WAT>
A; Cross-references: EMBL:273078; MIPS:YGR293c
A; Experimental source: strain S288C
C; Genetics:
                                               A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: SGD:S0003525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 27.0%
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: C49897; S36428
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 LCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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AB1543
AB1543
AB1543
B. subtilis YbtB protein homolog lin0882 [imported] - Listeria innocua (strain Clip11 C; Species Listeria innocua
C; Date: 137-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C; Accession: AB1543
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
S; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
Science 294, 849 852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Accession: AB1543
A; Molecule type: DNA
A; Residues: 1-494 GLA>
A; Coss-references: GB:AL52022; PIDN:CAC96114.1; PID:g16413332; GSPDB:GN00178
A; Genetics:
A;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1185
A;Status: preliminary
A;Wolecule type: DNA
A;Residues: 1-491 < CLA>
A;Coss-references: GB:NC_003210; PIDN:CAC98961.1; PID:g16410286; GSPDB:GN00177
A;Coss-references: Strain EGD-e
C;Genetics:
A;Gene: lmo0883
C;Superfamily: Bacillus subtilis hypothetical protein ydbT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 19.8%; Score 56; DB 2; Length 491 Best Local Similarity 28.6%; Pred. No. 24; Matches 12; Conservative 9; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 GLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLTLC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 GLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLTLC 53
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Best Local S
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                                                                                                                                                                                                    Districted chain alpha keto-acid dehydrogenase El alpha chain [imported] - Arabidopsis tha C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C. Accession: T51858
R. Mooney, B.P.; Miennyk, J.A.; Randall, D.D.
S. Mooney, B.P.; Miennyk, J.A.; Randall, D.D.
A. Reference number: 225485
A. Reference number: 225485
A. Reference number: 225485
A. Residue: preliminary; translated from GB/EMBL/DDBJ
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Status: anna
A. Residues: 1-472 canoo
A. Cross-references: EMBL: AF077955; PIDN: AAC69851.1
C. Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin
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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.I., C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C., A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Southwick, A.M.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A. Accession: A86447
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 1
C;Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1.472 <STO>
A;Cross-references: GB:AE005172; NID:g9454571; PIDN:AAF87894.1; GSPDB:GN00141
C;Genetics:
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AC1185
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Best Local Similarity 34.0%; Pred. No. 23;
Matches 16; Conservative 10; Mismatches 19; Indels
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|:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |: | |:: | 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Gaps

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 21, 2002, 13:42:31; Search time 10 Seconds (without alignments) 84.572 Million cell updates/sec Run on:

US-09-776-724A-142 Perfect score:

283 1 MRRCVRHVLGIGLIVLKNLY.....FQEAFLFFFLILKNPLTLCS 54 Sequence:

100480 segs, 15661496 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 35 Apply	Sequence 36. April	Segmence 58, April	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	20	Segmence 67. April		٤,	Segmence 160. Ann	Sequence 1300. An	Segmence 4 Appli	Segmence 7. Appli	Segmence 22. Appl	Sequence 24. Appl			` 4	Segmente 8 Aprellis	Sequence 7, Appli	
SUMMAKIES		ID	US-09-761-288-35	US-09-761-288-36	US-09-747-835A-58	US-09-761-288-4	US-09-761-288-38	US-09-761-288-67	US-09-761-288-89	US-08-910-386A-2	US-10-001-879-160	US-09-925-301-1300	US-09-745-763-4	US-08-910-386A-7	US-09-761-288-22	US-09-761-288-24	US-09-761-288-64	US-09-804-156-15	US-09-946-633-7	US-09-945-249-8	US-09-803-589-7	
		DB	10	10	10	10	10	10	10	8	12	10	10	æ	10	10	10	10	10	6	10	
		Match Length DB	260	260	304	310	310	310	310	612	91	96	216	1025	310	310	310	372	372	384	714	
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		Score	59	59	59	59	59	59	59	58.5	55.5	52.5	52.5	52.5	52	52	52	52	52	52	52	
	Result	No.	Т	7	3	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	

Sequence 252, App Sequence 4983, Ap Sequence 1344, Ap Sequence 1148, App Sequence 11020, Ap Sequence 110, App Sequence 117, Appl Sequence 17, Appl Sequence 26, Appl Sequence 270, App Sequence 214, Appl Sequence 214, Appl Sequence 114, Appl Sequence 115, Appl Sequence 114, Appl Sequence 115, Appl S	
10 US-09-801-368-252 10 US-09-815-24-4983 10 US-09-814-761-37449 10 US-09-764-864-1020 10 US-09-764-864-1020 10 US-09-764-864-1020 10 US-09-815-242-13946 10 US-09-815-243-11 10 US-09-918-243-11 10 US-09-918-249-9 10 US-09-978-249-9 10 US-09-978-249-9 10 US-09-978-249-9 10 US-09-978-249-9 10 US-09-978-249-9 10 US-09-978-249-9 10 US-09-978-249-9 10 US-09-978-249-9 10 US-09-86-118-269-91-919-919-919-919-919-919-919-919-91	0 US-09-841-132-180 0 US-09-740-668A-44
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18.2 18.0 17.7 17.7 17.3 17.3 17.3 17.3 17.3 17.3	17.1 17.0
11. 0 4 4444 444 9. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0.	48.5
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ALIGNMENTS

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APPLICANT: Padigaru, Muralidhara
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Taupler, Raymond J
APPLICANT: Taupler, Raymond J
APPLICANT: Mishra, Vishuu
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberky
APPLICANT: Li, Li
TITLE OF INVENTION: NO. US20020065405Alel Polypeptides and Nucleic Acids Encoding
FILE REPRENCE: 129566-638
GURRENT APPLICATION NUMBER: US709/761,288
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (152)...(165)
OTHER INFORMATION: Wherein Xaa is any amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/17/839
PRIOR PILING DATE: 2000-01-25
PRIOR PELING DATE: 2000-01-14
PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-13
PRIOR PLING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/218,324
PRIOR APPLICATION NUMBER: 60/218,324
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-07-26
PRIOR PELICATION NUMBER: 60/178,191
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/178,227
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/178,27
PRIOR PILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/178,27
PRIOR PILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/178,27
PRIOR PELING DATE: 2000-01-26
                               Sequence 35, Application US/09761288 Patent No. US20020065405A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35
LENGTH: 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                  GENERAL INFORMATION:
US-09-761-288-35
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LITTLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
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APPLICANT: Li, Li, Mo. US20020065405Alel Polypeptides and Nucleic Acids Encoding
TILLE OF INVENTION: NO. US20020065405Alel Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 15966-638
CURRENT APPLICATION NUMBER: US/09/761,288
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/177,839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 RTCFSHLCVIGLVYGTAIIMIVGPRYGNPK---EQKKXLLLFHSLFNPMLNPLICS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
                                  TITLE OF INVENTION: TELINOLS AND MALEALING TO S FROITENEY
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-37CIP
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT FILING DATE: 2002-03-08
PRIOR PADLICATION NUMBER: US 09/729,739
PRIOR PILING DATE: 2000-08-31
PRIOR PILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR PILING DATE: 2000-08-31
PRIOR PILING DATE: 2000-08-31
PRIOR PILING DATE: 2000-08-31
PRIOR PILING DATE: 2000-06-32
PRIOR PILING DATE: 2000-06-25
PRIOR PILING DATE: 2000-06-25
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR PILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
SOFTWARE PREAITING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
20.8%; Score 59; DB 10; Length 304;
Best Local Similarity 30.4%; Pred. No. 1.4;
Matches 17; Conservative 9; Mismatches 24; Indels
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PRIOR PILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/218,324
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/220,253
PRIOR PILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR APPLICATION NUMBER: 60/178,227
PRIOR FILING DATE: 2000-01-26
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PRIOR APPLICATION NUMBER: 60/176,134
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/175,989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09761288
Patent No. US20020065405A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Padigaru, Muralidhara
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Taupier, Raymond J
APPLICANT: Mishra, Vishnu
APPLICANT: Tchernev, Velizar
Drmanac, Radoje T
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-747-835A-58
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LENGTH: 304
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APPLICANT: Li, Li
TITLE OF INVENTION: No. US20020065405Alel Polypeptides and Nucleic Acids Encoding Sam
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                                                                                                                                                                    2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
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Pred. No. 1.2;
                                                   Score 59; DB 10; Length 260; Pred. No. 1.2;
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                                                                                                                   24; Indels
                                                                                                                   9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE COFINENTION: 0.520220004405ALEI FOIL RELEBERENCE: 15966-638
CURRENT APPLICATION NUMBER: US/09/761,288
CURRENT FILING DATE: 2001-01-16
PRIOR PAPLICATION NUMBER: 60/17,839
PRIOR FILING DATE: 2000-01-25
PRIOR PELING DATE: 2000-01-14
PRIOR PELING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/218,324
PRIOR APLICATION NUMBER: 60/218,324
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-01-26
PRIOR PILING DATE: 2000-07-25
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                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-761-288-36
Sequence 36, Application US/09761288
; Patent No. US20020065405A1
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Prayaga, Vadhirdas
APPLICANT: Taupier, Raymond J
APPLICANT: Mishra, Vishnu
                                                            20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 20.8%;
Local Similarity 30.4%;
les 17; Conservative 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tchernev, Velizar
Spytek, Kimberky
Li, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.0
                                                               Query Match 20.89
Best Local Similarity 30.49
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang, Jie
Ren, Feiyan
Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-761-288-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-747-835A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 36
LENGTH: 260
           US-09-761-288-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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| Patent No. US20020065405A1
| GENERAL INFORMATION:
| APPLICANT: Padigaru, Muralidhara
| APPLICANT: Padigaru, Muralidhara
| APPLICANT: Taupier; Raymond J
| APPLICANT: Saytek, Kimberky
| APPLICANT: Saytek, Kimberky
| APPLICANT: Saytek, Kimberky
| APPLICANT: Saytek, Mumber: 0009/161,288
| CURRENT APPLICATION NUMBER: 60/176,33
| PRIOR FILING DATE: 2000-01-13
| PRIOR FILING DATE: 2000-01-13
| PRIOR PELING DATE: 2000-01-13
| PRIOR APPLICATION NUMBER: 60/176,34
| PRIOR PELING DATE: 2000-07-14
| PRIOR PELING DATE: 2000-07-14
| PRIOR PELING DATE: 2000-07-24
| PRIOR PELING DATE: 2000-01-26
| PRIOR PELING DATE: 2000-07-25
| NUMBER OF SEQ ID NOS: 95
| SED ID NO S: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 RTCFSHLCVIGLVYGTAIIMYVGPRYGNPK---EQKKYLLLFHSLFNPMLNPLICS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.8%; Score 59; DB 10; Length 310; Best Local Similarity 30.4%; Pred. No. 1.5; Matches 17; Conservative 9; Mismatches 24; Indels
                         CURRENT PELICATION NUMBER: US/09/761,288
CURRENT FILING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-25
PRIOR PELING DATE: 2000-01-15
PRIOR PELING DATE: 2000-01-14
PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 2000-01-13
PRIOR PELICATION NUMBER: 60/218,324
PRIOR FILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR PILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/178,27
PRIOR APPLICATION NUMBER: 60/178,27
PRIOR PILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/220,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 89, Application US/09761288
; Patent No. US20020065405A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Homo sapiens US-09-761-288-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-761-288-89
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LENGTH: 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Prayaga, Sudhirdas
APPLICANT: Taupier, Raymond J
APPLICANT: Taupier, Raymond J
APPLICANT: Taupier, Neshar
APPLICANT: Echernew, Velizar
APPLICANT: Li, Li,
TITLE OF INVENTION: No. US20020065405Alel Polypeptides and Nucleic Acids Encoding Sam CURRENT APPLICATION NUMBER: US/09/761,288
CURRENT FILICATION NUMBER: US/09/761,288
PURPLY FILICATION DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: No. US20020065405Alel Polypeptides and Nucleic Acids Encoding Sam
                                                                                                                                                 2;
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                                                                                                                                                 6; Gaps
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                                                                                                                                                                                                                                                          238 RICESHLCVIGLVYGTAIIMYVGPRYGNPK---EQKKYLLFHSLFHSHFNPLICS 290
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                                                                                                                                                                                                           2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
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                                                                 Query Match 20.8%; Score 59; DB 10; Length 310; Best Local Similarity 30.4%; Pred. No. 1.5; Matches 17; Conservative 9; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.8%; Score 59; DB 10; Length 310; 30.4%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/177,839
PRIOR PELING DATE: 2000-01-25
PRIOR PELING DATE: 2000-01-16
PRIOR PELING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR PILING DATE: 2000-01-13
PRIOR PELING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/175,989
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/18,324
PRIOR PELING DATE: 2000-07-24
PRIOR PELING DATE: 2000-07-26
PRIOR PELING DATE: 2000-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38, Application US/09761288
Patent No. US20020065405A1
GENERAL INFORMATION:
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Patent No. US20020065405A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Padigaru, Muralidhara
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Taupier, Raymond J
APPLICANT: Mishra, Vishnu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      JS-09-761-288-38
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LENGTH: 310
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US-09-761-288-4
                                                                     Query Match
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Gaps

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2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1300, Application US/09925301 Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09745763 Patent No. US20020065394Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                            Query Match 19.6%;
Best Local Similarity 38.5%;
Matches 15; Conservative
 Cafferkey, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                 TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-879-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-09-925-301-1300
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US-09-745-763-4
                                                                                                                                                                                                                               SEQ ID NO 160
LENGTH: 91
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                             2;
                                                                                                                                                         2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Hibber, Soct
APPLICANT: Richter, Todd
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resisitance in Plants
CORRESPONDENCE: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.7%; Score 58.5; DB 8; Length 612; 38.3%; Pred. No. 3.7;
                                                   Score 59; DB 10; Length 310;
Pred. No. 1.5;
                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA.
APPLICATION VUMPER: US/08/910,386A FILING DATE: 13-AUG-1997
                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Finbarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                           9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 023070-058950US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 160, Application US/10001879
Patent No. US20020127237A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                 Sequence 2, Application US/08910386A Patent No. US20020092041A1 GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02.
TELECOMMUNICATION INFORMATION:
                                                     20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    612 amino acids
                                                                                             Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Conservative
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; ORGANISM: Homo sapiens US-09-761-288-89
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                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: USA
94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-001-879-160
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                                                                                                                                                                                                                               RESULT 8
US-08-910-386A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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APPLICANT: Ali, Shujath
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a
FILE REFERENCE: DEX-0281
CURRENT APPLICATION NUMBER: US/10/001,879
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 6//252,188
PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 201
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Treacy, Maurice
Spaulding, Vikk
TITLE OF INVENTION: SECRETED PROFEINS AND POLYNUCLEOTIDES
ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIOS

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: PATENTIN NUMBER: 6/124,270

NUMBER OF SEQ ID NOS: 1694

SEQ ID NO 1300

LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                     Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 12;
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RESULT 14
US-09-761-288-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLTLCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Ronald, Pamela C.
APPLICANT: Ronald, Pamela C.
APPLICANT: Song, Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Hulbert, Scot
APPLICANT: Richter, Todd
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resisitance in Plants
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18 -Jun-2000
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/910,386A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 18.6%; Score 52.5; DB 10; Best Local Similarity 25.9%; Pred. No. 7; Matches 14; Conservative 14; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                            ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Springer, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08910386A Patent No. US20020092041A1
                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 216 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
NUMBER OF SEQUENCES: 219 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Bastian, Kevin L.
                                                                                                                                             COUNTRY: U.S.A. ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                    STATE: MA
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                                                                                                                                                                      DB 8; Length 1025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.4%; Score 52; DB 10; Length 310; 29.6%; Pred. No. 12; tive 8; Mismatches 24; Indels
                                                                                                                                                                    18.6%; Score 52.5; DB 8; Length 1 36.2%; Pred. No. 42; tive 6; Mismatches 19; Indels
                                                                                                                                                                                                                                    1 MRRCVRHVLGIGLIVLKNLYFHKNSM---YPSP--KLSSFQEAFLFF 42
RECISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058950US
TELECOMMUTICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09761288
Patent No. US20020065405A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                              Prayaga, Sudhirdas
Taupier, Raymond J
Mishra, Vishnu
                                                                                           1025 amino acids
                                                                                                                                                                                Best_Local Similarity 36.2
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 29.6
Matches 16; Conservative
                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                       amino acid
                                                                                                                   TOPOLOGY:
                                                                                                                                           US-08-910-386A-7
                                                                                                                                                                                                                                                                                              US-09-761-288-22
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LENGTH: 310
                                                                                           LENGTH:
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APPLICANT:
                                                                                                                                                                      Query Match
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PRIOR APPLICATION NUMBER: 60/178,191
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-761-288-64
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                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: No. US20020065405alel Polypeptides and Nucleic Acids Encoding Sam FILE OF INVENTION: No. US20020065405alel Polypeptides and Nucleic Acids Encoding Sam FILE REPRENCE: 15966-638

CURRENT APPLICATION NUMBER: US/09/761,288

CURRENT FILING DATE: 2001-01-16

PRIOR FILING DATE: 2000-01-13

PRIOR FILING DATE: 2000-01-14

PRIOR FILING DATE: 2000-01-14

PRIOR FILING DATE: 2000-01-13

PRIOR FILING DATE: 2000-01-13

PRIOR FILING DATE: 2000-01-26

PRIOR FILING DATE: 2000-01-26

PRIOR FILING DATE: 2000-01-26

PRIOR PLICATION NUMBER: 60/178,191

PRIOR FILING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: 60/178,27

PRIOR APPLICATION NUMBER: 60/178,27

PRIOR PLING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: 60/178,27

PRIOR PILING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: 60/178,27

PRIOR APPLICATION NUMBER: 60/178,27

PRIOR APPLICATION NUMBER: 60/178,27

PRIOR APPLICATION NUMBER: 60/120,590

PRIOR APPLICATION NUMBER: 60/220,590

PRIOR APPLICATION NUMBER: 60/220,590
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APPLICANT: TCHETO, VEHIZAR
APPLICANT: SPYTEK, Kimberky
APPLICANT: SPYTEK, Kimberky
APPLICANT: Li, Li
TITLE OF INVENTION: NO. US20020065405Alel Polypeptides and Nucleic Acids Encoding Sam
FILE REFERENCE: 15966-638
CURRENT APPLICATION NUMBER: US/09/761,288
CURRENT APPLICATION NUMBER: G0/177,839
PRIOR APPLICATION NUMBER: 60/177,839
PRIOR PILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.4%; Score 52; DB 10; Length 310; Best Local Similarity 29.6%; Pred. No. 12; Matches 16; Conservative 8; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 64, Application US/09761288; Patent No. US20020065405A1; GENERAL INFORMATION: APPLICANT: Padigaru, Muralidhara APPLICANT: Prayaga, Sudhirdas APPLICANT: Taupier, Raymond J. APPLICANT: Mishra, Vishnu
Sequence 24, Application US/09761288; Patent No. US20020065405A1; GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara; APPLICANT: Prayaga, Sudhirdas; APPLICANT: Taupier, Raymond J. APPLICANT: Mishra, Vishpu
                                                                                                                                                                                                                                                                            APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberky
APPLICANT: Li, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-761-288-24
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                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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18.4%; Score 52; DB 10; Length 310;
Best Local Similarity 29.6%; Pred. No. 12;
Matches 16; Conservative 8; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: November 21, 2002, 13:46:13 Job time : 10 secs
PRIOR FILING DATE: 2000-0126
PRIOR APPLICATION NUMBER: 60/178,227
PRIOR FILING DATE: 2000-0126
PRIOR APPLICATION NUMBER: 60/20,590
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PATENTIN Ver. 2.0
: SEQ ID NO 64
: LENGTH: 310
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(without alignments)
113.488 Million cell updates/sec
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283
1 MRRCVRHVLGIGLIVLKNLY......FQEAFLFFFLILKNPLTLCS
                                                                                                    November 21, 2002, 13:40:51; Search time 14 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                          262574 seqs, 29422922 residues
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	62 Sequence 362, App	480 Sequence	Sequence 24	4 Sequence 24.	4	4 Sequence 24,	9 Sednence 66,	99	Sequence 12,	~	Sequence 2,	Sequence 4.	4	Sequence 4,	Sequence 19.	19,	Sequence 19.	19,	ď	7	7	Sequence 2,	Sequence 15,	7		, ,	, , ,
SUMMARIES	ID	US-09-149-476-36	-001	9	09-299-843A-	US-09-088-337B-2	-US93-11153-	US-09-299-843A-6	US-09-088-337B-6	S-09-108-020-1	US-08-180-371-2	05707	US-08-475-891A-4	US-08-567-375-4		US-08-153-848-19	US-09-299-843A-1	US-09-088-337B-1	593	-90	-09-178-	-08-383	-08-383-751A-	-08-153	-08-352	US-09-299-843A-1	US-09-251-545-1	119-00-015-502-10
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Sequence 15, Appl	Sequence 49, Appl	2. A	Sequence 15, Appl	7,7	7	7	7	8	9	ė		Sequence 3, Appli	10,	7	18,	3.	Sequence 67, Appl
US-09-088-337B-15	US-09-534-185-49	PCT-US93-09636-2	PCT-US93-11153-15	US-08-153-848-7	US-09-299-843A-7	US-09-088-337B-7	PCT-US93-11153-7	US-08-477-451-8	US-09-198-956-6	US-09-670-141-6	US-09-025-580-3	US-08-904-871-3	US-08-726-214-10	US-09-473-716-2	US-08-185-432-18	US-08-899-232-3	US-09-413-814-67
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378	378	378	378	410	410	410	410	3200	415	415	422	009	1098	1261	2523	2523	2890
18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.2	18.0	18.0	18.0	18.0	18.0	18.0	18.0	18.0	18.0
52	52	52	52	52	52	52	52	51.5	51	51	51	51	51	51	51	51	51
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

EARLIER FILLION DUMBER: 0()017,500
EARLIER FILLION DUMBER: 0()017,587
EARLIER FILLION DUMBER: 0()017,587
EARLIER FILLION DUMBER: 0()017,693
EARLIER FILLION DATE: 1997-05-23
EARLIER FILLION DATE: 1997-05-23
EARLIER FILLION DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 0()017,582
EARLIER APLICATION NUMBER: 0()017,582
EARLIER FILLION DATE: 1997-05-23
EARLIER FILLION DATE: 1997-06-13
EARLIER FILLION DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 0()043,569
EARLIER FILLION DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 0()043,569
EARLIER FILLION DATE: 1997-04-11
EARLIER FILLION DATE: 1997-04-12
EARLIER FILLION DATE: 1997-04-12
EARLIER FILLION DATE: 1997-04-12
EARLIER FILLION DATE: 1997-04-13
EARLIER FILLION DATE: 1997-04-13
EARLIER FILLION DATE: 1997-04-13
EARLIER FILLION DATE: 1997-06-22
EA

ER APPLICATION NUMBER: 00/030,042)

ER APPLICATION NUMBER: 00/056,892

ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22

ER PELICATION NUMBER: 00/047,595

ER PILING DATE: 1997-05-23

ER APPLICATION NUMBER: 00/047,595

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 00/047,586

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 00/047,586

ER FILING DATE: 1997-05-23

ER PELING DATE: 1997-05-23

ER PELICATION NUMBER: 00/047,590

ER FILING DATE: 1997-05-23

ER PELICATION NUMBER: 00/047,590

ER ELING DATE: 1997-05-23

ER PELICATION NUMBER: 00/047,593

ER FILING DATE: 1997-05-23

ER FILING DATE: 1997-05-23

ER FILING DATE: 1997-05-23

ER PELICATION NUMBER: 00/047,593

ER FILING DATE: 1997-05-23

ER PELICATION NUMBER: 00/047,614 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/057,650
FILING DATE: 1997-09-05
APPLICATION NUMBER: 60/056,884
FILING DATE: 1997-08-22 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/056,632
FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881
FILING DATE: 1997-08-22
APPLICATION UNMBER: 60/056,909
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,875 APPLICATION NUMBER: 60/043,578 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,501 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,862
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,887
FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,908 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/048,964 APPLICATION NUMBER: 60/056,664 FILING DATE: 1997-08-22 BARLIER I BARLIE EARLIER DE SERLIER DE EARLIER FEARLIER FEARLIER EARLIER A BARLIER PARLIER BARLIER EARLIER EARLIE EARLIER EARLIER

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APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwelkart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56; DB 1; Length 359;
Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago CITY: Lllinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
                  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/153,848 FILING DATE: 17-NOV-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/977,452 FILING DATE: 17-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                             US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/09299843A Patent No. 6107475 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH 359 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 19.8
Best Local Similarity 32.6
Matches 14; Conservative
                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-24
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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MEDIUM TYPE: Floppy
                                                                                    FILING DATE: CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60606
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-108-14
NUMBER OF SEQ ID NOS: 5674

EENGTH: 673
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                                                                                                                                                                                                                                                       1 MRRCVRH-VLGIGLIVLKNLYFHKNSMYPS-----PKLSSFQEAFL-FFFLIL 46
                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                Query Match
22.8%; Score 64.5; DB 4; Length 132;
Best Local Similarity 37.5%; Pred. No. 0.057;
Matches 21; Conservative 9; Mismatches 9; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 20.7%; Score 58.5; DB 4; Length 673; Best Local Similarity 32.3%; Pred. No. 2.9; Matches 20; Conservative 7; Mismatches 14; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
AITLE OF INVENTION: NO. 5759804el Seven Transmembrane
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6300 Sears Tower, 233 South Wacker Drive
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-134-001C-4480
S-26quence 4480, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Staphylococcus epidermidis US-09-134-001C-4480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/08153848 Patent No. 5759804 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
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4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL 46
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ADDRESSEE:
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US-09-299-843A-66
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                                                                                                                                   PCT-US93-11153-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Godiska, Ronald
Godiska, Patrick W.
Schwelkart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                    Query Match 19.8%; Score 56; DB 3; Length 359; Best Local Similarity 32.6%; Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                         4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                                                                                                                                49 CFVGLLGNGLVILTYIYFKRLKTMTDTYLLNLAVADILFLLIL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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RAPLICATION NUMBER: US/09/088,337B
APPLING DATE: 01-Jun-1998
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: No. 6348574and, Greta E. REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 359 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
TELECOMMUNICATION INFORMATION:
                                                                          INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
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                TELEFHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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Best Local Similarity 32.6
Matches 14; Conservative
                                                                                                                                                                                                                                                                                 Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60606
                                                                                                                                                                linear
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Gaps
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Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                          Sequence 24, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Vartick W.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL 46
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49 CFVGLLGNGLVILTYIYFKRLKTMTDTYLLNLAVADILFLLIL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NOland, Greta E.
REGISTRATION NUMBER: 35,302
REFINENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPANNE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         Chicago
: Illinois
XY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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Gray, Patrick W.
Schweikart, Vioki L.
IITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 19.8%; Score 56; DB 3; Length 378; Local Similarity 32.6%; Pred. No. 3.4; es 14; Conservative 7; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 CFVGLLGNGLVILTYIYFKRLKTMTDTYLLNLAVADILFLLIL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL 46
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                   SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27866/32059B
                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/299,843A
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 66, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
                                                                                                                                                 COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 27:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60606
COMPUTER READABLE FORM:
                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 378 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                        Illinois
                 Chicago
                                                              USA
                                                                                90909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-299-843A-66
                                                                                                                                                                                         SOFTWARE:
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STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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GENERAL INVENCENTION

STATEMENT: BANDAILOM

APPLICANT: Johnston, Mark L.

APPLICANT: Johnston, Mark L.

APPLICANT: Michael H.

APPLICANT: Michael H.

APPLICANT: Michael H.

APPLICANT: Money, Brian P.

TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE AND TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO CURRENT FILING DATE: 1998-06-30

EARLIER APPLICATION NUMBER: 60/055,255

EARLIER FILING DATE: 1997-06-30

EARLIER FILING DATE: 1997-06-30

EARLIER FILING DATE: 1997-08-01

EARLIER FILING DATE: 1997-08-01

EARLIER FILING DATE: 1998-03-02

NUMBER: OF SEQ ID NOS: 54

COMMINABER: DELACATION NUMBER: 60/076,544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.8%; Score 56; DB 4; Length 378; 32.6%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 CFVGLLGNGLVILTYIYFKRLKTMTDTYLLNLAVADILFLLIL 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Mismatches
                                                                                                   FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO: 63485/4and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
                                                                            APPLICATION NUMBER: US 08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 66: US-09-088-337B-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09108020A Patent No. 6143561 GENERAL INFORMATION:
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 378 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Arabidopsis thaliana US-09-108-020-12
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Best Local Similarity 34.0%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-09-108-020-12
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RESULT 10

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GENERAL INFORMATION:
APPLICANT: Choudhury, Chandra
APPLICANT: Choudhury, Chandra
TITLE OF INVENTION: Hematopoietic Growth Factor Derived
TITLE OF INVENTION: from T
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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GENERAL INFORMATION:
APPLICANT: Choudhury, Chandra
TITLE OF INVENTION: Hematopoietic Growth Factor Derived from
TITLE OF INVENTION: T Lymphocytes and Methods of Use Therefor
NUMBER OF SEQUENCES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 VPFQNIFWESVTESSHQTLSTFEPRLXXTFFQKHYLXFICLVTSPLSLCS 436
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CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PAIGHT, F. D. D. M. Wersion #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/180,371
FILING DATE: 12-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 906866
FILING DATE: 01 July 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27620/31668
                                                                                                                                                                                                                                                                                                  STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-180-371-2; Sequence 2, Application US/08180371; Patent No. 6254861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 37,060
REFERENCE/DOCKET NUMBER: 27,1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 554 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-180-371-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                 Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US92-05707-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Gaps
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APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.6%; Score 55.5; DB 5; Length 554; 26.0%; Pred. No. 6.4; tive 13; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 VPFQNIFWFSVTESSHQTLSTFEPRLXXTFFQKHYLXFICLVTSPLSLCS 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 IVLKNLYF-----HKNSMYPSPKLSS--FQEAFLFFFLILKNPLTLCS 54
            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05707
FILING DATE: 19920707
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: U$/08/475,891A FILING DATE: 06-JUN-1995 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: U$ 08/373,375 FILING DATE: 17-JAN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor STRTE: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02370-058910US
                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 27620/30933
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEX: (312) 984-9740
TELEX: (312) 984-9740
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08475891A Patent No. 5859339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                 : 554 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 26.0%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-05707-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ronald, Pamela C.
APLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Indels
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6; Mismatches 19; Indels
                                                                                                   1 MRRCVRHVLGIGLIVLKNLYFHKNSM---YPSP--KLSSFQEAFLFF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
FILIG DATE: 17-JAN-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.6%; Score 52.5; DE
ilarity 36.2%; Pred. No. 36;
Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 023070-058940US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION: 00.0

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-DAN-1995
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA: 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
ATPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08587680A Patent No. 5977434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1025 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
      17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: TWO EMULACIONAL STREET: TWO EMULACIONAL COTY: San Francisco charte: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-587-680A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                            DB 2; Length 1012;
                                                                                                                                                                           /note= "Xa21 Xanthomonas spp.
disease resistance polypeptide RRK-B
from rice (Oryza sativa)"
                                                                                                                                                                                                                                                                                                                                      Query Match 18.6%; Score 52.5; DB 2; Length 1 Best Local Similarity 36.2%; Pred. No. 36; Matches 17; Conservative 6; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRRCVRHVLGIGLIVLKNLYFHKNSM---YPSP--KLSSFQEAFLFF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,375 FILING DATE: 04-DEC-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bastian, Kevin L. REGISTARTION UNDBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058930
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08567375
Patent No. 5952485
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
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36.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-567-375-4
                                                                                                                           ; OTHER INFORMATION: ); OTHER INFORMATION: defense of the control of control 
             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Embarcad
CITY: San Francisco
STATE: California
                                                                                                                    NAME/KEY: Protein
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                              FEATURE:
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5

Gaps

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Sequence 19, Application US/08153848
Parent No. 575904
Parent Gady Parink W
PAPICANT: Gady Parink W
PAPICANTON BAR SET TOWER TOWER W
PAPICANTON NOWER: US/08/153,848
PAPICANTON NOWER: S140
PAPICANTON NOWER: S140
PAPICANTON NOWER: S120
PAPICANTON
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Search completed: November 21, 2002, 13:43:12 Job time : 16 secs

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(without alignments)
205.587 Million cell updates/sec
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283
1 MRRCVRHVLGIGLIVLKNLY......FQEAFLFFFLILKNPLTLCS 54
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                 908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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a. Geneseq_101002:* 1. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* 2: /SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:* 3: /SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:* 4: /SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:* 5: /SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:* 6: /SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:* 7: /SIDS2/gcgdata/geneseqy-embl/AA1986.DAT:* 8: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1980.DAT:* 9: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1980.DAT:* 10: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1980.DAT:* 11: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 12: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 13: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 14: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 15: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 16: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 17: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 18: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 18: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 19: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 20: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 21: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 22: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 23: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 23: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 23: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 23: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:* 23: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA2002.DAT:* 23: /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Secreted protein e	Human nervous syst	Human secreted pro	Human reproductive	Human reproductive	Novel prostate gla	Novel prostate gla	Human polypeptide	Arabidopsis thalia	Arabidopsis thalia
SUMMARIES				701442	317898	474772	496017	496695	118865	118919	AA006321	347243	347242
~,			Ω	AA	ABI	AAI	AAI	AAI	AA	AAI	AA(AA(AA(
			DB	20	22	19	22	22	22	22	22	21	21
			Match Length DB	54	82	132	88	88	8	88	66	237	251
	dР	Query	Match	100.0	25.8	22.8	22.6	22.6	22.6	22.6	21.2	21.0	21.0
			Score	283	73	64.5	64	64	64	64	09	59.5	59.5
		Result	No.	17,	7.85.7	3	4	r.	9	7	8	6	10
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Arabidopsis thalia Human olfactory re Human olfactory re Human olfactory re Human olfactory re O. longistaminata Staphylococcus epi Human colon specif Arabidopsis thalia Arabidopsis thalia Human polypeptide Human polypeptide Human polypeptide Seven transmembran Murine 77M recepto Mouse 7 transmembra Arabidopsis branch Ilsteria monocytog Human polypeptide Human polypeptide Murine 77 transmembra Arabidopsis branch Listeria monocytog Human polypeptide	Human ORFX protein Human G protein-co Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia
AAG47241 AAU05132 AAG71441 AAG71441 AAG71441 AAU91143 AAU91143 AAU9125 AAG72954 AAG72954 AAG72954 AAG729565 AAG729565 AAG72965 AAG72965 AAG72965 AAG72965 AAG72965 AAG72965 AAG72965 AAG7296 A	ABP00261 AAU19189 AAG28190 AAG28189 AAG28188 AAG28188
12222222222222222222222222222222222222	23 21 21 20 20
3307 3100 3100 3110 3110 3100 3100 3100	62 199 200 228 312 1757
+000000000000000000000000000000000000	199.4 199.4 199.3 199.3
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ALIGNMENTS

Secreted protein encoded by gene 60 clone HOSDK95. AAY01442 standard; Protein; 54 AA. 18-MAY-1999 (first entry) AAY01442; RESULT 1 AAY01442

Human; secreted protein; gene therapy; protein therapy; cancer; weight; tumour; chromosome mapping; forensic; haematological disease; allergy; inflammation; cell proliferation; viral infection; wound healing; modulation; appetite; behaviour; food additive; preservative.

Homo sapiens

WO9903990-A1

28-JAN-1999.

97US-0052661. 97US-0052870. 97US-0052871. 97US-0052872. 98WO-US14613 97US-0056361 16-JUL-1997; 16-JUL-1997; 16-JUL-1997; 16-JUL-1997; 15-JUL-1998; 18-AUG-1997;

970S-0052873. 970S-0052874. 970S-0052875. 970S-0053440. 970S-0053441. 16-JUL-1997; 16-JUL-1997; 16-JUL-1997; 22-JUL-1997; 22-JUL-1997;

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The invention relates to nucleic acid sequences (AAX22211 to AAX22282)

cncoding human secreted proteins (AAY01383 to AAY01454). The secreted

cncoding human secreted proteins (AAY01383 to AAY01454). The secreted

cncoding man sequences are deposited with the ATCC under deposit number

ATCC 200138, 209139 or 209141. Host cells containing vectors comprising

the nucleic acid sequences are used for the recombinant expression of

the secreted proteins. The polynucleotide and amino acid sequences are

useful for preventing, treating or ameliorating medical conditions can

by protein or gene therapy. Pathological conditions can be also diagnosed

by determining the amount of the new polyneptides in a sample or by the

crossence of mutations in the new polynucleotides. The nucleic acid

sequences, or its fragments, are useful for chromosome identification

crossence of mutations in the new polynucleotides. The nucleic acid

sequences, or its fragments, are useful for chromosome identification

crossence of mutations in the new polynucleotides. In gene

therapy; for (forensic) identification of individuals; as molecular

cuseful as immunoassay reagents (including for in vivo imaging) and

charpentically to inhibit or activate particular polypeptides. A very

wide range of disorders may be treated with the polynucleotide and

conther infections. The sequences may also be useful in wound healing,

cro modulate differentiation of embryonic stem cells, to modulate weight,

cappetite, behaviour etc. and as food additive or preservative. The

present sequence represents human secreted protein (see describtor

con the for gene number and clone identification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                              New nucleic acids encoding secreted human proteins - potentially useful for treating and diagnosing diseases and identifying specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQBAFLFFFLILKNPLTLCS
                                                                                                                                                           Ferrie AM, Florence KA, Fouad J;
Ni J, Rosen CA, Ruben SM, Young PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human nervous system related polypeptide SEQ ID NO 6555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 283; DB 20;
100.0%; Pred. No. 5.4e-34;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                              Claim 11; Page 233; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB17898 standard; Protein; 85
                     970S-0055724.
970S-0055725.
970S-0055726.
970S-0055946.
970S-0055952.
                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
 97US-0053442
            97us-0055683
                                                                                    97us-0055985
                                                                                                97us-0055989
                                                                                                             97US-0056359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                          WPI; 1999-132234/11.
N-PSDB; AAX22270.
                                                                                                                                                            Feng P, 1
M, Hu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 AA;
                                                                                                                                                                                                                                                                       binding agents
                                                                      18-AUG-1997
18-AUG-1997
                         18-AUG-1997
                                   18-AUG-1997
                                                18-AUG-1997
                                                            18-AUG-1997
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                                                                                                                                                                        Greene JM,
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immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antiparkinsonian; hepatchropic; cerebroprotective; antiflammatory; antiallergic; antidiabetic; antiunconvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
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2000US-0186350
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                                                                                                                                                Homo sapiens.
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18-APR-2000;
19-MAY-2000;
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16-MAR-2000;
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2000US-0246611.
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2000US-0249207.
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08-DEC-2000;
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17-NOV-2000;
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26-SEP-2000;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. In the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chaemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial schaemias; (d) wound healing; (e) neurological diseases us, erebral anoxia and epilepsy; and (f) infectious diseases such as wirel, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                     Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; testis; tumour; foetal brain tissue; fusion protein; cancer; central nervous system; seizure; diagnosis; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 6555; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.8%; Score 73; DB 22; Length 85; 30.5%; Pred. No. 0.0068; tive 11; Mismatches 16; Indels
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                                                                                                                                                          Ruben SM;
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                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                 08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
                  2000US-0251869.
2000US-0251989.
   2000US-0251868
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Best Local Similarity 30.2.,
...ac 18; Conservative
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                                                                                                                                                                                         WPI; 2001-541565/60.
N-PSDB; ABA14224.
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08-DEC-2000; 2
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970S - 004 0336
970S - 004 3312
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07-MAR-1997;
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07-MAR-1997;
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07-MAR-1997;
11-APR-1997;
123-MAY-1997;
133-MAY-1997;
132-MAY-1997;
132-MAY-1997;
132-MAY-1997;
132-MAY-1997;
132-MAY-1997;
133-MAY-1997;
14-MAG-1997;
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152-MAG-1997;
152-MAG-1997;
153-MAG-1997;
153-MAG-199
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22-AUG-1997
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This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 43 from the human cDNA clone HSNBB14 (deposited as clone ATCC 97899 and ATCC 209045).

The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fe portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleated acid sequences: AAV55511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypucleotides, Specific uses are described for each of the 186 conditions can be diagnosed which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
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9705-0056862.
9705-005684.
9705-0056874.
9705-0056875.
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97US-0056911.
97US-0057650.
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97US-0057761.
97US-0058785.
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22-AUG-1997
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22-AUG-1997
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22.8%; Score 64.5; DB 19; Length 132; 37.5%; Pred. No. 0.21; Live 9; Mismatches 9; Indels 17; Gaps

21; Conservative

Matches

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Query Match Best Local Similarity Ŋ

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Human; reproductive system related antigen; reproductive system disorder;
                                                                                                   Human reproductive system related antigen SEQ ID NO: 4675.
                        AAM96017 standard; Protein; 89 AA
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20000S-0225757.
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20000S-0226279.
20000S-0226681.
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2000US-0227009.
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2000US-0229287.
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                                                                         21-NOV-2001 (first entry)
                                                                                                                                             cancer; gene therapy
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08-SEP-2000;
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07-JUN-2000;
28-JUN-2000;
                                                                                                                                                                     Homo sapiens
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16-MAR-2000;
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18-APR-2000;
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PR 20-OCT-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249211
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                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a reproductive system antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                              used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 4675; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           22.6%; Score 64; DB 22; Length 89; 60.0%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human reproductive system related antigen SEQ ID NO: 5353.
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                                                                                                                                                                                                Ruben SM;
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11-DEC-2000; 2000US-0251990.
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32-JUN-2000; 2000US-0214886.
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| 13 LIVLKSFFFFKDSLTPSPRL 32
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                                                                                                                                                                                                                                                                                                                                                                                                89 AA;
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13 LIVLKNLYFHKNSMYPSPKL 32
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18-AUG-2000;
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Pred. No. 0.15;
5; Mismatches 3; Indels
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Human; nootropic; neuroprotective; cytostatic; antiparkinsonian; antianaemic; dermatological; immunosuppressive; antinflammatory; antirhemmatic; virucide; hepatotropic; nephrotropic; osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; antoimmune disorder; skin aging; systemic lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       liver disorder; wound healing; food preservative.
                                                                                                                                                                                                                                                                                                               Novel prostate gland antigen, Seq ID No 164.
                                                                                                                                                      AAU18865 standard; Protein; 89 AA
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2000US-0224519.
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29-SEP-2000; 2000US-023637.
20-CCT-2000; 2000US-0237038.
20-CCT-2000; 2000US-0237038.
20-CCT-2000; 2000US-0237039.
20-CCT-2000; 2000US-023935.
13-CCT-2000; 2000US-0241785.
20-CCT-2000; 2000US-0241786.
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20-CCT-2000; 2000US-024186.
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08-NOV-2000; 2000US-0246524.
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08-NOV-2000; 2000US-0246611.
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Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 164; 512pp; English.
                                                                                                                                                                                                                                         Rosen CA, Barash SC, Ruben SM;
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The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, proposition, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, granulomatous prostatitis, malacoplakia, benign prostatic prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic hypertrophy or hyperplasia, and prostate neoplastic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas, (I), (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget's disease), autoimmune disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (sickle cell anaemia), hyperproliferative disorders, unionary system disorders (arrhythmias), cardiovascular disorders (arrhythmias), cardiovascular disorders (arrhythmias), and neurological disorders (Alzheimer's disease and Parkinson's disease), endocrine disorders (Alzheimer's disorders (arrhythmias), and neurological disorders (Alzheimer's disorders) cand neurological disorders (Alzheimer's disorders) cand neurological disorders (Alzheimer's disorders), pancreatic and gall bladder disorders, disorders of the large intestine, pancreatic and gall bladder disorders, disorders of the large intestine, developmental and inherited disorders, disorders of the large intestine, and wound healing and epithelial cell proliferation. (I) or (II) is

Gaps ó 22.6%; Score 64; DB 22; Length 89; 60.0%; Pred. No. 0.15; Live 5; Mismatches 3; Indels Local Similarity 60.0 nes 12; Conservative Query Match Matches

13 LIVLKNLYFHKNSMYPSPKL 32 δy

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RESULT 7

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antianaemic; dermatological; immunosuppressive; antiinflammatory; antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic; osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; beniqu prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; autoimmune disorder; urinary system; system; lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder; liver disorder;
                                                                                                                                                       Human; nootropic; neuroprotective; cytostatic; antiparkinsonian;
                                                                                                                        Novel prostate gland antigen, Seq ID No 218.
                 AAU18919 standard; Protein; 89 AA
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14-AUG-2000; 2000US-0225213.
14-AUG-2000; 2000US-0225214.
14-AUG-2000; 2000US-0225267.
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14-AUG-2000; 2000US-025268.
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16-MAR-2000; 2000US-0189874.
17-MAR-2000; 2000US-0199874.
19-MAY-2000; 2000US-0198123.
19-MAY-2000; 2000US-0205515.
07-JUN-2000; 2000US-020465.
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2000US-0215135.
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04 NOV - 2000; 2000US - 0246474.
08 NOV - 2000; 2000US - 0246475.
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08 NOV - 2000; 2000US - 02464776.
08 NOV - 2000; 2000US - 0246478.
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08 NOV - 2000; 2000US - 024651.
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                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
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AA006321 standard; Protein; 99 AA.

06-NOV-2001 (first entry)

AA006321;

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to vytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity in in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 59523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.2%; Score 60; 41.7%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG47243 standard; Protein; 237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 PKLSSFQEAFLFFFLILKNPLTLC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000US-0515126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514838/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAI86252
                                                                                                                                                                                               WO200164835-A2
                                                                                                                                           Homo sapiens.
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31-AuG-1999)
31-AuG-1999)
01-SEP-1999)
10-SEP-1999)
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04 - JUN - 1999;
08 - JUN - 1999;
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99US-0142055.
99US-0142390.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 - JUN-1999;
     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                              Score 59.5; DB 21; Length 237; Pred. No. 2.3; 8; Mismatches 14; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 59522.
                                                                                                                                                                                                                                                                                                                                                                                                           168 GVGCMTAKILRFHQESLNELSQLLQYSSFKFFFFFFYNIV 207
                                                                                                                                                                                                                                                                                                                                                                                              10 GIGLIVLKNLYFHKNSMYPSPKL---SSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG47242 standard; Protein; 251 AA.
99US-0154779.
99US-0155139.
99US-0155486.
                                 990S-0156458
990S-01567636
990S-0157717
990S-0157753
990S-0157865
990S-0158029
990S-0158029
990S-0159293
990S-0159294
990S-0159329
990S-0159330
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99US-0159584.
99US-0160741.
99US-0160767.
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99US-0160980.
99US-0160981.
                                                                                                                                                                                                                                                                                           99US-0161359.
99US-0161360.
99US-0161361.
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1 Similarity 37.5%;
15; Conservative E
                                                                                                                                                                                                                                                                                                                    99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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99US-0160814
                                                                                                                                                  99US-0159331
99US-0159637
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99US-0161406
                                                                                                                                                                                                                                                                   99US-0161404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0121825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 15; Conserval
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                        24-SEP-1999;
28-SEP-1999;
04-0CT-1999;
05-0CT-1999;
06-0CT-1999;
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28-0CT-1999;
28-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                    28-OCT-1999;
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21-70L-1999;
22-70L-1999;
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-JUL-1999;
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16-AUG-1999;
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19-JUL-1999
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                             Length 251;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 59521.
                                                                                                                                                                                                                                                                                                                                                             Score 59.5; DB 21;
Pred. No. 2.4;
8; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                 10 GIGLIVLKNLYFHKNSMYPSPKL---SSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                                                                                                                                                                                                AAG47241 standard; Protein; 307 AA
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99US-0123180.
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99US-0126264.
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99US-0126285.
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37.5%;
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990S-0160814
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990S-0161359-
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990S-0161992-
990S-0161993-
990S-0161993-
990S-0161993-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                               Query Match 21.04
Best Local Similarity 37.54
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
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09-MAR-1999;
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21-0CT-1999;
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16 - APR - 1999 16 - APR - 1999 21 - APR - 1999 23 - APR - 1999 23 - APR - 1999 24 - ARY - 1999 30 - APR - 1999 30 - APR - 1999 30 - APR - 1999 30 - APR - 1999 31 - ARY - 1999 32 - ARY - 1999 33 - APR - 1999 34 - ARY - 1999 35 - ARY - 1999 36 - ARY - 1999 37 - ARY - 1999 38 - ARY - 1999 39 - ARY - 1999 30 - ARY - 1999 31 - ARY - 1999 31 - ARY - 1999 32 - ARY - 1999 33 - ARY - 1999 34 - ARY - 1999 36 - ARY - 1999 37 - ARY - 1999 38 - ARY - 1999 39 - ARY - 1999 39 - ARY - 1999 31 - ARY - 1999 32 - ARY - 1999 33 - ARY - 1999 34 - ARY - 1999 35 - ARY - 1999 36 - ARY - 1999 37 - ARY - 1999 38 - ARY - 1999	23-700-199 28-700-199 28-700-199 29-700-199 01-701-199 01-701-199 01-701-199 01-701-199 01-701-199 01-701-199 01-701-199 01-701-199 01-701-199 01-701-199 01-701-199 01-701-199 01-701-199
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90S-0144333 90S-0144334 90S-0144335 90S-0144635 90S-0144884 90S-0144884 90S-0145086 90S-0145086 90S-0145086 90S-0145089	9075 - 014 522 9075 - 014 522 9075 - 014 591 9075 - 014 591 9075 - 014 591 9075 - 014 591 9075 - 014 918 9075 - 014 918	
9-JUL-1- 9-JUL-1- 9-JUL-1- 0-JUL-1- 0-JUL-1- 1-JUL-1- 1-JUL-1- 1-JUL-1- 22-JUL-1- 22-JUL-1- 22-JUL-1- 3-JUL-1- 3-JUL-1- 3-JUL-1-	3 - JUL - 199 3 - JUL - 199 3 - JUL - 199 7 - JUL - 199 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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us-09-776-724a-142.rag

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The sequence represents the amino acid sequence of human odorant receptor (OR)-like protein, NOV2. The NOV2 polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOV2 polypeptide. The NOV2 nucleic acid and polypeptide are especially useful in therapeutic or prophylactic acids for disorders of the neuro-olfactory system, e.g. those induced by trauma, surgery and/or neoplastic disorders. The DNA encoding the protein is useful in gene therapy for treating the above conditions. Furthermore, the nucleic acids and polypeptides are
                                             New NOVX polypeptides and polynucleotides, useful for treating or preventing disorders of the neuro-olfactory system, cancer and multiple
                                                                                                                                                                                                                                                              useful in treating adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune response, acquired immunodeficiency syndrome (AIDS), asthma, Crohn's disease, multiple sclerosis or Albright hereditary osteodystrophy. These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
                                                                                                                                                                                                                                                                                                                                                                                      20.8%; Score 59; DB 22; Length 310; 30.4%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human olfactory receptor polypeptide, SEQ ID NO: 1122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glusman G,
                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG71441 standard; Protein; 310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lancet D,
                                                                                                     Claim 1; Page 16; 141pp; English
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(YEDA ) YEDA RES & DEV CO LTD.
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24-FEB-2000; 2000US-0184809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-2000; 2000WO-US27582.
                                                                                                                                                                                                                                                                                                                                      in diagnostic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.47
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-290713/30.
         WPI; 2001-451859/48.
                                                                                                                                                                                                                                                                                                                                                               310 AA;
                     N-PSDB; AAS09946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                            sclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Odorant receptor; human; OR; NOV2; therapeutic; neuro-olfactory system; trauma; surgery; neoplastic disorder; gene therapy; adenocarcinoma; lymphoma; prostate cancer; uterus cancer; immune response; asthma; AIDS; acquired immunodeficiency syndrome; Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                 21.0%; Score 59.5; DB 21; Length 307; 37.5%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                      238 GVGCMTAKILRFHQESLNELSQLLQYSSFKFFFFFYNIV 277
                                                                                                                                                                                                                                                                                                                                                                                                                     10 GIGLIVLKNLYFHKNSMYPSPKL --- SSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human odorant receptor (OR)-like protein, NOV2.
                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU05132 standard; Protein; 310 AA.
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2000US-0220253.
2000US-0220590.
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2000US-0178191.
2000US-0178227.
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99US-0160815.
99US-0160980.
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99US-0160989.
99US-0161404.
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99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161920.
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                                                               99US-0159638
                                                                                                                                  99US-0160770
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                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 15; Conserv
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26-JAN-2000;
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Spytek KA,
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29-OCT-1999;
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28-OCT-1999
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                          14-0CT-1999
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26-0CT-19
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14-0CT-1
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25-0CT-1
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AAU05132
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Gaps

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Yanai I;

Fuchs T,

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The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods of the odour receptors used to detect these primary scents. The methods combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
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                                                                                                                                                                                                                                                                                                                                                                                                        2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS
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Pred. No. 3.7;
9; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human olfactory receptor polypeptide, SEQ ID NO: 1153.
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Claim 11; Page 646-647; 1857pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG71472 standard; Protein; 310 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES & DEV CO LTD.
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30.4%;
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24-FEB-2000; 2000US-0184809.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                           Query Match 2003
Best Local Similarity 30.49
Watches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-290713/30.
                                                                                                                                                                                                                                                                                                  310 AA;
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                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods sto enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to

Claim 11; Page 672-673; 1857pp; English.

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The present invention relates to the isolation of novel human genes designated PHORI-All and PHORI-F5D6 and their encoded proteins. The gene encoding PHORI-All maps to chromosome 1q23, and the gene encoding PHORI-F5D6 maps to chromosome 7q33-q35. The PHORI-All and PHORI-F5D6 polynucleotide and polypeptide sequences are useful in diagnostic and therapeutic methods, and compositions for various cancers such as prostate cancer. The sequences are useful for inhibiting the growth of cancer cells that express PHORI-All or PHORI-F5D6 and for treating cancer. The PHORI-All or PHORI-F5D6 polypeptide or a fragment thereof can be used to elicit an immune response. The present sequence represents
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re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of cancer in subject, by determining status of PHORI-AII/PHORI-F5D6 gene products in tissue sample from subject and comparing it to normal sample
                                                                                                                                                           6; Gaps
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                                                                                                                                                                                                              238 RICFSHLCVIGLVYGTAIIMYVGPRYGNPK---EQKKYLLLFHSLFNPMLNPLICS 290
                                                                                                                                                                                     2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
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9
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                                                                                                                        DB 22; Length 310; 3.7; thes 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; PHOR1-A11; PHOR1-F5D6; prostate cancer; cytostatic.
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                                                                                                                                                       9; Mismatches
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                                                                                                                        Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                             Human PHOR1-F5D6 amino acid sequence.
                                                    faculties of different individuals.
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                                                                                                                                                                                                                                                                                                          AAU91543 standard; Protein; 310 AA
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                                                                                                                        20.8%;
                                                                                                                                      30.48;
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                                                                                                             Query Match
Best Local Similarity 30.49
Matches 17; Conservative
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                                                                                      310 AA;
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                                                                                        Sequence
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Db 238 RTCFSHLCVIGLVYGTAIIMYVGPRYGNPK---EQKKYLLLFHSLFNPMLNPLICS 290

Search completed: November 21, 2002, 13:41:32 Job time : 37 secs

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